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1	6	cory NEAR suzanne	USPAT;	2004/03/29 14:36
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15	97	(bcl NEAR w) and apoptosis	USPAT;	2004/03/29 14:38
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			EPO; JPO;	
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	1		EPO; JPO;	
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18	10	(US-5883229-\$ or US-5789201-\$).did. or	USPAT;	2004/03/29 14:40
		(US-20020119943-\$ or	US-PGPUB;	
		US-20040014218-\$).did. or (WO-9735971-\$ or	EPO;	
		WO-9914321-\$ or WO-9913710-\$ or	DERWENT	
		WO-9115116-\$).did. or (WO-9913710-\$ or		1
	L	US-20020119943-\$).did.		<u></u>

Page 1

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FILE 'MEDLINE, CANCERLIT, SCISEARCH, CAPLUS' ENTERED AT 14:42:01 ON 29
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            124 S E11
1.1
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             10 DUP REM L5 (19 DUPLICATES REMOVED)
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     ANSWER 3 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
L7
     1997:650444 CAPLUS
ΑN
DN
     127:327462
     A novel mammalian gene, bcl-w, belongs to the
ΤI
     bcl-2 family of apoptosis-controlling genes
     PCT Int. Appl., 85 pp.
     CODEN: PIXXD2
     Cory, Suzanne; Adams, Jerry McKee; Gibson, Leonie M.; Holmgreen,
ΙN
     Shaun P.
     Human and mouse cDNAs for bcl-2-related gene bcl-
AB
     w and the corresponding proteins are disclosed. The present
     invention is broadly directed to therapeutic mols. capable of inter alia
     modulating apoptosis in mammalian cells. The therapeutic mols. of the
     present invention encompass genetic sequences and chemical entities capable
     of regulating expression of bcl-w family and which
     promotes cell survival. The therapeutic mols. of the present invention
     may have further utility in delaying cell cycle entry. In addition, the
     present invention extends to chemical entities capable of modulating activity
     and function of the translation product of the bcl-w
     gene. The present invention also extends to the translation product of
     the bcl-w gene and its use in, for example, therapy,
     diagnosis, antibody generation and, as a screening tool for therapeutic
     mols. capable of modulating physiol. cell death or survival and/or
     modulating cell cycle entry. The bcl-w gene was
     mapped to human chromosome 14q11.2. Alternative splicing of the
     bcl-w gene transcript produced an mRNA for a bcl
     -w-rox chimera. The bcl-w gene was
     expressed in many cell types. Amongst the tissues surveyed, the level was
     highest in brain, colon and salivary gland. A survey of 50 mouse
     hemopoietic cell lines revealed that bcl-w expression
     was common in cells of several myeloid lineages, including macrophage,
     megakaryocyte, erythroid and mast cell lines, but rare in either B or T
     lymphoid lines.
     PATENT NO.
                       KIND DATE
                                              APPLICATION NO. DATE
                                                                19970327
                       A1 19971002
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     WO 9735971
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A1 19990804
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     ANSWER 8 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
1.7
     1999:215553 CAPLUS
AN
DN
     130:235990
     Animals carrying bcl-w mutations and their use in the
     study of male infertility
SO
     PCT Int. Appl., 52 pp.
     CODEN: PIXXD2
     Cory, Suzanne; Adams, Jerry; Print, Cris; Gibson, Leonie;
IN
     Koentgen, Frank
     Transgenic mice carrying a disruption of the bcl-w
AR
     gene or of genes interacting with it and that fail to undergo productive
     spermatogenesis and are male infertile are described for use in studies of
     male fertility and of the biol. role of bcl-w. Such
     animals can be used to screen for therapeutic mols. including genetic
     sequences capable of inducing, enhancing or otherwise facilitating
     spermatogenesis in said animals as well as a model for mols. and genetic
     sequences which can induce infertility. The bcl-w
     gene was disrupted by insertional inactivation. Inactivation of
     bcl-w did not affect survival of fetal and neonatal mice
     and the mutation showed a near-normal Mendelian segregation.
     Hematopoiesis was unaffected by the mutation but the testes showed
     heterogeneous pathol. changes in the seminiferous tubules. Sertoli cells
     remained normal although low in number and Leydig cell were increased by 50%.
     Germ cell nos. declined steadily with as the stage of development
     advanced. The mutation did not affect androgen levels or androgen
     responses in other organs.
                      KIND DATE
                                            APPLICATION NO. DATE
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                                          WO 1998-AU764 19980916
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     ANSWER 1 OF 10
                         MEDLINE on STN
L7
                  MEDLINE
AN
     96358615
     bcl-w, a novel member of the bcl-2 family,
TI
     promotes cell survival.
     Oncogene, (1996 Aug 15) 13 (4) 665-75.
SO
     Journal code: 8711562. ISSN: 0950-9232.
     Gibson L; Holmgreen S P; Huang D C; Bernard O; Copeland N G; Jenkins N A;
ΑU
     Sutherland G R; Baker E; Adams J M; Cory S
     The prototypic mammalian regulator of cell death is bcl-2, the
AB
     oncogene implicated in the development of human follicular lymphoma.
     Several homologues of bcl-2 are now known. Using a PCR-based
     strategy we cloned a novel member of this gene family, denoted bcl
     -\mathbf{w}. The gene, which is highly conserved between mouse and
     human, resides near the T-cell antigen receptor alpha gene within the
     central portion of mouse chromosome 14 and on human chromosome 14 at band
     q11. Enforced expression of bcl-w rendered lymphoid
     and myeloid cells refractory to several (but not all) cytotoxic
     conditions. Thus, like Bcl-2 and Bcl-x, the
     Bcl-w protein promotes cell survival, in contrast to
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other close homologues, Bax and Bak, which facilitate cell death. Comparison of the expected amino acid sequence of Bcl-w with that of these relatives helps to delineate residues likely to convey survival or anti-survival function. While expression of bcl-w was uncommon in B or T lymphoid cell lines, the mRNA was observed in almost all murine myeloid cell lines analysed and in a wide range of tissues. These findings suggest that bcl-w participates in the control of apoptosis in multiple cell types. Its functional similarity to bcl-2 also makes it an attractive candidate proto-oncogene.

- L7 ANSWER 4 OF 10 MEDLINE on STN
- AN 1998445387 MEDLINE
- TI Apoptosis regulator **bcl-w** is essential for spermatogenesis but appears otherwise redundant.
- Proceedings of the National Academy of Sciences of the United States of America, (1998 Oct 13) 95 (21) 12424-31.

  Journal code: 7505876. ISSN: 0027-8424.
- AU Print C G; Loveland K L; Gibson L; Meehan T; Stylianou A; Wreford N; de Kretser D; Metcalf D; Kontgen F; Adams J M; Cory S
- Proteins of the Bcl-2 family are important regulators of AΒ apoptosis in many tissues of the embryo and adult. The recently isolated bcl-w gene encodes a pro-survival member of the Bcl-2 family, which is widely expressed. To explore its physiological role, we have inactivated the bcl-w gene in the mouse by homologous recombination. Mice that lack Bcl- ${f w}$  were viable, healthy, and normal in appearance. Most tissues exhibited typical histology, and hematopoiesis was unaffected, presumably due to redundant function with other pro-survival family members. Although female reproductive function was normal, the males were infertile. The testes developed normally, and the initial, prepubertal wave of spermatogenesis was largely unaffected. The seminiferous tubules of adult males, however, were disorganized, contained numerous apoptotic cells, and produced no mature sperm. Both Sertoli cells and germ cells of all types were reduced in number, the most mature germ cells being the most severely depleted. The bcl-w-/- mouse provides a unique model of failed spermatogenesis in the adult that may be relevant to some cases of human male sterility.
- L7 ANSWER 7 OF 10 MEDLINE on STN
- AN 1999310955 MEDLINE
- TI Survival activity of Bcl-2 homologs Bcl-w and Al only partially correlates with their ability to bind pro-apoptotic family members.
- SO Cell death and differentiation, (1999 Jun) 6 (6) 525-32. Journal code: 9437445. ISSN: 1350-9047.
- AU Holmgreen S P; Huang D C; Adams J M; Cory S
- Certain Bcl-2 family members promote cell survival, whereas AΒ others promote apoptosis. To explore further how heterodimerization of opposing members affects survival activity, we have compared the abilities of the anti-apoptotic Bcl-w and Al to bind to the pro-apoptotic Bax, Bak, Bad and Bik and to protect cells from their cytotoxic action. Bcl-w co-immunoprecipitated from cell lysates with Bax, Bak, Bad and Bik, but Al bound only Bak and Bik. Mutation of Al at a highly conserved glycine within the BH1 domain prevented binding, but the comparable Bcl-w mutant still bound Bak, Bad and Bik, indicating that the glycine is not essential for all heterodimerization. Bcl-w and Al protected against apoptosis induced by over-expression of Bax or Bad but not that induced by Bak or Bik. With several gene pairs, binding and protection were discordant. The results may reflect critical threshold affinities but also suggest that certain pro-apoptotic proteins may also contribute to apoptosis by a mechanism independent of binding pro-survival proteins.
- L7 ANSWER 9 OF 10 MEDLINE on STN
- AN 2001360165 MEDLINE
- TI Tissue expression and subcellular localization of the pro-survival molecule Bcl-w.
- SO Cell death and differentiation, (2001 May) 8 (5) 486-94.

Journal code: 9437445. ISSN: 1350-9047.

AU O'Reilly L A; Print C; Hausmann G; Moriishi K; Cory S; Huang D C; Strasser A

Anti-apoptotic members of the Bcl-2 family, such as Bcl AB -w, maintain cell viability by preventing the activation of the cell death effectors, the caspases. Gene targeting experiments in mice have demonstrated that Bcl-w is required for spermatogenesis and for survival of damaged epithelial cells in the gut. Bcl-w is, however, dispensable for physiological cell death in other tissues. Here we report on the analysis of Bclw protein expression using a panel of novel monoclonal antibodies. Bcl-w is found in a diverse range of tissues including colon, brain and testes. A survey of transformed cell lines and purified hematopoietic cells demonstrated that  ${\tt Bcl-w}$  is expressed in cells of myeloid, lymphoid and epithelial origin. Subcellular fractionation and confocal laser scanning microscopy demonstrated that  $\mathbf{Bcl\text{-}w}$  protein is associated with intracellular membranes. The implications of these results are discussed in the context of the phenotype of Bcl-w-null mice and recent data that suggest that Bcl-w may play a role in colon carcinogenesis.

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## AL I GNMENT

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AX022529
apoptosis-controlling genes Patent: EP 0932674-A 6 04-AUG-1999;	A novel mammalian gene, bcl $^{\sim}$ $_{ m W}$ , belongs to the bcl-2 family of	Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.		unclassified.	unidentified	unidentified	•	AX022529.1 GI:10046125	AX022529	Sequence 6 from Patent EP0932674.	AX022529 583 bp DNA linear PAT 07-SEP-2000	

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/db_xref="GI:10046126"
/db_xref="GI:10046126"
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GAALCAES/NKEMEPLYGQVQEWMYAYLETRLVDWIH8SGGWABFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/mol_type="unassigned DNi
/db_xref="taxon:32644"
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/db_xref="GI:10278312"
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/db_xref="taxon:32644"
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Adams, J.M.

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Euteleostomi; Homo.

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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Cory,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-JUN-1996) Molecular Biology Uni
Eliza Hall Institute of Medical Research, PO
Hospital, Parkville, Victoria 3050, Australia
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Mammalia; Eutheria;
1 (bases 1 to 582)
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                                                                                                                  GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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 AGTGGGGGGGGGGGGGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG
                                                         CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACCGCGGCTGGTCGACTGGATCCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="promotes cell survival"
/codon_start=1
/product="Bcl-w"
/protein_id="AAB09055.1"
/protein_id="AAB09055.1"
/db_xref="GI:1572493"
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AMRAAGDEFETRERETFSDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVF
GAALCABSVNKEMEPLYGQVOEMVNAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
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Pred. No. 4.8e-120;
0; Mismatches 3;
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Human mRNA :
D87461
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                                                                                                                       μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:Containfoskazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
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Ohara, O., Nagase, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                       AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
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                                                                                  ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
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                                                                                                                                                                                                                                                              /proteIn_id="BAA19666.1"
/db_xref="GI:1944418"
/db_xref="GI:1944418"
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GAALCAESVNIEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="KIAA0271"
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="KIAA0271"
177, .758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="myloblast"
/tissue_type="brain"
/clone_lib="psporT 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HA6752"
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                                                                                                                                                           Score 575; DB 9; Pred. No. 1.2e-119; 0; Mismatches 5;
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Guastella,J.

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/mol_type="unassigned
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Rattus no
AF096291
                                                                                                                                                                                                                                                                                                                                                                       Hamner, S., Skoglosa, Y. and Lindholm, D. Direct Submission
Submitted (01-OCT-1998) Developmental Submitted (7-0 E87 BMC, Uppsala 751
                                                                                                                                                                                                                                                                                                                                                      University, Box 587, BMC, Upp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamner,S., Skoglosa,Y. and Lindholm,D. Differential expression of bcl-w and bcl-x developing and adult rat nervous system Neuroscience 91 (2), 673-684 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
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Eukaryota; Metazoa
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 /product="mb01-w"
/protein_id="mac64200.1"
/protein_id="mac64200.1"
/db xref="G1:3747130"
/translation="MATPASTPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQ
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AMRAAGDEFETERRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNMGRLVAFFVF
GAALCAESVNKEMBEJVGQVQDMWTYLETRADWIHSSGGMAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                       /codon_
                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                            gene="bcl-w"
                                                                                                                                                                                              gene="bcl-w"
                                                                                                                                                                                                                               tissue_type="brain"
dev_stage="postnatal"
                                                                                                                                             note="Bcl-2
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2 (bases 1 to 1110)
Itoh,T., Itoh,A. and Pleasure,D.
Direct Submission
Submitted (21-NOV-2002) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center 516 I, 3517 Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                        Itoh, T., Itoh, A. and Pleasure, D.
Bcl-2-related protein family gene expression
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
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Pred. No. 7.7e-109;
0; Mismatches 34;
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mRNA

linear

ROD

24-JUN-2003

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480

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420 360 360

420

300

240 240 180 180 120

300

ORIGIN

/organism="Rattus

norvegicus"

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AY185098.1 GI:32185280
                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                      Rattus norvegicus (Norway
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
431. .1090
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/protein_id="AAO64470.1"
/db xref="GI:32185285"
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, B., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
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Eliza Hall Institute of Medical Research, PO I
Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                                TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                                                              CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
 AGTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGGACGGGGCCCCTGGAGGAGGCGCGG
                                                                                                                                                                CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                             AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCCAGCCGGAC
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/protein id="AAB09056.1"
/protein id="AAB09056.1"
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GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVCAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="promotes cell survival;
/codon_start=1
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/mol_type="mRNA"
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/chromosome="14"
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93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 522.8; DB 10;
Pred. No. 9.4e-108;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
AF030769
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Submitted (21-OCT-1997) Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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                                                                                                                                                                               /codon_start=1
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GAALCAESYNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                                                         /note="mRNA destabilization 3428. .3441
                                                                                                                                                                    RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                              179. .760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/10J"
/db_xref="taxon:10090"
/chromosome="14"
                                                                                       3356. .3364
/gene="Bcl-w"
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                                                                                                                                      'gene="Bcl-w"
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   Score 522.8;
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mRNA,
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                                                                                                                                                                                                                                                                                                                                                                          3473 bp mRNA
Mus musculus Bcl2-like protein 2 mRNA,
AY170344
      Submitted (22-SEP-2003) Biotechnology, Pingtung University, Hsueh Fu Road, Nei-Pu Hslang, Pingtung, Taiwan 912, Taiwan Sequence update by submitter On Sep 22, 2003 this sequence version replaced gi:27497698.

Location/Qualifiers
1. 3473
                                                                                                                         Direct Submission
Submitted (29-OCT-2002) Biotec
Hsueh Fu Road, Nei-Pu Hsiang,
3 (bases 1 to 3473)
                                                                                                 Direct Submission
                                                                                                               Su, H. -Y
                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                      Extraction from neonatal mouse
                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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0; Mismatches
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siang, Pingtung,
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Sequence 8 from I
AX022531
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GAALCAESVNKHMEPLVGQVQDWMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFAYK"
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/strain="C57BL"
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/dev_stage="neonatal"
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A novel mammalian gene, bol-w, belongs to
apoptosis-controlling genes
Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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/proteain_id="CAC07881.1"
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/db_xref="taxon:32644"
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LOCUS DEFINITION ACCESSION RESULT 14 AX022531

SOURCE KEYWORDS VERSION

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Matches 531; Conservative (
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A novel mammalian gene, bcl-w, belongs to the bcl-2 family
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-CCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZA
ADAMS JERRY MCKEE (AU); AMRAD OPERATIONS PTY LTD (AU)
; GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
Location/Qualifiers
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GRALCARSVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALVGDGALEDAR
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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GGGGCCCTGGTAACTGTAGGGGCCTTTTTTTGCTAGCAAGTG 581

Search completed: March 29, 2004, 06:11:55 Job time: 2776.74 secs

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AW258810 CB790932

CB749817

BF785386 602111728
CB578463 AMGNNUC:N
AKO13244 Mus muscu
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CA407899 1004048 H
BU557268 AGENCOURT
BU557410 AGENCOURT
AW258810 um74a02:y
CB799932 AMGNNUC:N
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CB749816 BY704881
BY704881 BY704881
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BY740551 BY704881
CF538813 WI-M-FY0-BG6718 CD6878466718
CB667345 602624059
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CF538813 UI-M-FY0-BG6718
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AA596919 V021f08 F
B0646339 AGENCOURT
BY285647 BY285647
BY253191 BY253191
AW326901 20104 MAR
CB760687 AMGNNUC:N
AA596919 BY253191
AW326901 20104 MAR
CB760687 AMGNNUC:N

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BY253189 CB786193

ALIGNMENTS

**BY251598** 

CA984774

AW326901 CB760687 BB856021 CA984774 BY312773 CF282823 CF374729 BY2511598 BY253169 CB786193 BY356166

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BY253189
AMGNNUC:N
BY356166

BB856021 AGENCOURT

PUBMED REFERENCE AUTHORS 2 (bases 1 to 582)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 582)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003) AY421020.1 GI:39776977 Homo sapiens BCL2L2 gene, Homo sapiens (human) 14671302 Submission survey sequence. 582 bp DNA rricu., VIRTUAL TRANSCRIPT, partial sequence, GSS 17-DEC-2003

Result No.

Score

Match Length Query

DB

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Description

JOURNAL

TITLE

SUMMARIES

572.4 550 548.4 522.8

98.2 94.3 94.1 89.7

582 804 1030 582

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AL157542 AL157542 BE793530 BAY421022

AY421020 Homo sapi AL157542 DKFZD761D BE793530 601590016 AY421022 Mus muscu

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Wiemann, S.)

Berlin. 6, 1405

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Rockville, MD 20850,
This sequence as made
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 804)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemar
                                                                                                               AL157542 804 bp mR)
DKFZD761D0816 r1 761 (synonym: hamy2)
DKFZD761D0816 5', mRNA sequence.
AL157542
AL157542.1 GI:7057943
                                                                                     Homo sapiens
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1...>582
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/locus_tag="HCM7418"
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                                                                                      (human)
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Pred. No. 1.5e-120;
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Unpublished (1999)
Contact: MIPS
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This clone (DKFZp761D0816) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
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                                                 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA
                                                                  GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA
                                                                                                            CGTCTGCGGGAAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTGGCACT-
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/db_xref="taxon:9606"
/clone="bxF2p7=610816"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Si
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Pred. No. 2.3e-115;
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LICM800 row: p column: 04
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Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1030)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                          AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
                                                                                                                                                                                                                        CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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                                                                                     CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
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//lab host="DH108 (phage-resistant)"
//lab host="DH108 (phage-resistant)"
//clone lib="NIH MGC 7"
//clone lib="NIH MGC 7"
//note="Organ: lūng; Vector: pOTB7; Site 1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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cell_line="MGC3"
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Best Local Similarity
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      CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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Science 302 (5652), 1960-1963 (2003)
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Mus musculus BCL2L2 gene,
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Mammalia; Eutheria;
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This sequence as made by sequencing genomic exons and ordering them
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    Conservative
                                                                                                               /gene="BCL2L2"
/locus_tag="HCM7418"
                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:10090"
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Score 522.8; DB 29;
Pred. No. 3.4e-109;
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                                               Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsurra, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                  Genome Res.
20530913
11076861
                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashitzaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930488D08 product:Bcl2-like 2, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gecriken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1949)
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Mammalia; Eutheria;
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Pred. No. 5.8e-109;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Cenome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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6 (bases 1 to 3487)
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                                                                                                                                                                                                      organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                      /dev_stage="adult"
209. _.790
                                                           /tissue_type="lung"
/clone_lib="RIKEN_full-length
                                                                                                                                                                                                                                                                Gocation/Qualifiers
    note="unnamed protein
                                                                                                         'sex="male"
                                                                                                                                                             db_xref="FANTOM_DB:1200009L24"
db_xref="MGI:1896837"
                                                                                                                       clone="1200009L24"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 969)
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GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASURTVLTGAVALGALVTVGAFFASK"
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93.6%;
                                                                       (house mouse)
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Pred. No. 7.6e-109;
D; Mismatches 37;
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Bource

/organism="Mus musculus" /mol type="mRNA" /strain="C57BL/6J" /db\_xref="taxon:10090"

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COMMENT
FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., KOjima,Y.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., KOjima,Y.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Nokamura,M.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Nurata,M., Sakto,R., Sakazume,N.,
Nomura,K., Numazaki,R., Ohno,M., Oheato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
Contact: For Genome Exploration Research Group, RIKEN
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia; real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to the contributed to the
                                                                                                                                    prepare mouse tissues.
Please visit our web
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                                                                                details.
Location/Qualifiers
                                                                                                                                           web site (http://genome.gsc.riken.go.jp) for
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Pred. No. 9.9e-109;
0; Mismatches 38;
                   bp mRNA linear 2017 - 1 sapiens cDNA clone IMAGE:5209862 5',
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TITLE
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Matches 542;
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High quality sequence stop: 695.
Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMN1526 row: k column: 15
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                ACAAGTGCAGGAGTGGATGGGCCTACCT-GGAGACGCGGCTGGTCGACTGGATCCACA 418
                                                                                                                                                                                                           CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
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  GTCTTTGGGGCTGCACTGTGTTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGG
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/note="Organ: pooled lung and spleen; Vector: pcMV-SPORT6;
/note="Organ: pooled lung and spleen; RNA source
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
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db_xref="taxon:9606"
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|lab_host="DH10B"
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98.0%;
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Primates;
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Pred. No. 3.9e-100;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
Contact: Baken
                                             121
                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14043 row: c column: 23
High quality sequence stop: 524.
Location/Qualifiers
1 0677
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BU503850

967 bp mRNA lines AGENCOURT 10030867 NIH_MGC_94 Mus musculus cDNA 5', mRNA sequence.

BU503850
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                                                                                                                                                                                                                                                          Similarity
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                                         CCGCTGCAACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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           ccecrecaccaneceareceecirecresasaceaerireasacceerriceeceececace
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/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 Mb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                        79.9%;
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Pred. No. 5.4e-96;
0; Mismatches 39
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Clone IMAGE:6491566
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CR391923
CR30C9 y1 Human Retinal pigment (Un-normalized, unamplified): cs 5', mRNA sequence.
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                                                                                                                                                                                                                           Email: graeme@helix.nih.gov
plate: 20 row: c column: 09
Seq primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           National Eye Institute 6/331, NIH, Bethesda, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                        Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                 Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                          12107410
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/tissue_type="RPE/choroid"
/dev stage="Adult"
/dev stage="Adult"
/lab_host="EMDHIOS"
/clone_lib="Human Retinal pigment epithelium/choroid
/clone_lib="Human Retinal pigment epithelium/choroid
/clone_lib="Human Retinal pigment epithelium/choroid
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(Un-normalized, unamplified); cs"
(Un-normalized, unamplified); Two different
/note="Organ: Eye; Vector: pcMvsBoRT6; Two different
/note="Organ: Eye; Vector: pcMvsBoRT6; Two different
eyes (75-80 years old) yielded approximately 600 mg o
                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs20c09"
                                                                                                                                                                       organism="Homo sapiens"
/mol_type="mRNA"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MG: Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can |
                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC
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0; Mismatches
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60.2111728F1 NCI_CGAP_Kid14 Mus n
5', mRNA sequence.
BF785386
BF785386.1 GI:12090422
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    Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                  Mus musculus (house mouse)
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/OCDE="Vector: pCMV-SPORT6; Site_1: NOT1; Site_1....../
(destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leukocyte"
/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="IMAGE:5218294"
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Pred. No. 4.4e-85;
0; Mismatches 29;
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Gaps

199

60

REFERENCE AUTHORS TITLE JOURNAL COMMENT

SOURCE ORGANISM

Homo sapiens (human)

ACCESSION VERSION

BI910270.1 mRNA sequence.

GI:16173653

475

419

499

359

439 300 379

240 319 180 259 120

KEYWORDS

RESULT 11 BI910270 LOCUS

DEFINITION

603069493F1 NIH\_MGC\_118

BI910270

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ORIGIN

Query Match Best Local Similarity Matches 446;

76.0%; 98.7%;

Conservative

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JOURNAL COMMENT REFERENCE AUTHORS TITLE

FEATURES

source.

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L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9863 row: h column: 07
High quality sequence start: 3
High quality sequence stop: 650.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
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                                                                                                                            CACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGGGCGTCTGCGGGAGGGGAACTG
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                                                                                                     CACAGCTCTATACGGGGACGGGCCCTGGAGGAGGCACGG-GTCTGCGGGAGGGGAAC-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:4239798"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="NCI CGAP Kid14"
/clone lib="NCI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not /note= 2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
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/strain="FVB/N"
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Pred. No. 2.6e-80;
0; Mismatches 40;
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Amgen Rat EST Program
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Mammalia; Eutheria;
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/mol type="mRNA"
/db_xref="rtaxon:10116"
/clone="nrdg1-00100-h10"
/tissue type="borsal Root Ganglia"
/clone Tib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1;
dorsal root ganglia"
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Submitted (10-UUI-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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854 bp mRNA linear HTC 20-SEP-200: Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810435A13 product:Bcl2-like 2, full inser
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Best Local Similarity 91.7%;
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Gro
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CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420
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                                                 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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AMRAAGDEFETRERTFSDLAAQLHVTEGSAQQRFTQVSDELFQGGENWGRLVAFFVF
GBALCAESVNKEMBEPLVGGVQDWMVAYLETRLADWIHSSGGWVRSSQLLLSASLYKVG
LHGKIGPLMGGWGCAGRG"
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/clone Tib="RIKEN full-length enriched mouse cDNA library"
/dev stage="10, 11 days embryo"
196. 7.732
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/protein_id="BAB28740.1"
/db_xref="GI:12850488"
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/strain="C57BL/6J"
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Pred. No. 2.3e-75;
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AUTHORS
TITLE
JOURNAL
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Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I
1 (bases 1 to 792)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG298789 792 bp m
602396527F1 NIH_MGC_94 Mus musculus
mRNA sequence.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10394 row: e column: 08
High quality sequence stop: 713.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
                                                                                     CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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                                                 CAGGITTCCGACGAACITTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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/tissue_type="retina"
/lab_host="DH103 (phage-resistant)"
/clone_lib="NDH108 (phage-resistant)"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_i: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Sylte_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 %b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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Sciurognathi; Muridae; Murinae; Mus.
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AGTGGGGGCTGGTAAGA 534
                             AGTGGGGGCTGGGCGGA 437
                                                             CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 517
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Search completed: March 29, 2004, 07:28:08 Job time : 2302.9 secs

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Minimum DB
Maximum DB
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Aav28334 Human bcl
Aax15946 CDNA enco
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Aav28333 Rat bcl-y
Aax25943 CDNA enco
Aax25133 Mouse bcl
Aat96578 Mouse bcl
Aax25135 Mouse bcl
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Aax25136 Human sec
Abs73617 Human cDN
Acd82760 CDNA sequ
Abl32229 Human imm
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Add56779 Human	Abt16641 Human	줐	$\circ$	Aas15189 Human	Aaz93614 Bcl-x	Aat40079 Bcl-XL	œ	Aah43464 cDNA	9	Ade85177 Farnesyl	Abt09346 Phase	Aaf75960 Rat	Abs13513 Human	Aai05940 Probe	σ	Aak13683 Human	Aak39424 Human	Aba32370 Probe	Aba47382 Human	Aai45438 Probe	Aba65269 Human

## ALIGNMENTS

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RESULT 1

AAT96577

ID AAT9

XX AAT9

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XX Huma

XX Huma

XX Homo

XX NO97

XX WP01:

XX Nucl

XX This

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CC Surv

                                                                                                                                                                                                                                                                                           diseases.
                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative
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P-PSDB; AAW36047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cory s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
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                                                                                                                                                                                                                 Claim 3; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1996;
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/product= "bcl-w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibson LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmgreen
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This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human

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RESULT 2
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Matches 583
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                                                                                                                                                                             Spermatogenesis; bcl-3 animal model; ss.
                                                                                                                                                                                                                                                            Human
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llarity 100.0%;
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                                                                                                                                                                                                          gene;
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Pred. No. 7.3e-1
                                                                                                                                                                                                          Bcl-2;
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Query Match Best Local S Matches 583

Similarity

100.0%;

Score 583; DB 2; 1 Pred. No. 7.3e-136; ; Mismatches 0;

Length 0 Other;

Indels

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Gaps

583;

Conservative

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Sequence 583

BP; 105 A; 157 C;

210 G; 111 T; 0 U;

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481 421 421

CGTCTGCGGAAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG

540 480 480 420 420 360 360

CTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG

AGTGGGGGCTGGGCGAGTTCACAGCTCTATACCGGGGACGCGCCCTGGAGGAGGACGCCCCG CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC

481

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CAGGTCTCCGACGACTTTTTCAAGGGGGCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC TICTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC ccecrecadecadecareceeecadecreeaeareaerreeaeareaecreeaeceecace CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCCCTTCCGGCGCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGGCCCAGCAGCTGAC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT

CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCCAAC

TGGGGCCGCCTTGTAGCCTTCTTT

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The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival comember of the Bcl-2 family which is widely expressed and which is comessed and experimental for spermatogenesis. The invention relates generally to a complex that is and to an animal model for the identification of complex and genetic sequences useful for inducing or reducing fertility of molecules and genetic sequences useful for inducing or reducing fertility, confined the sequences of the sequences of infertility, confirmed the sequences of the sequences of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised companies tubules and are substantially infertile, but possess no other companies of inducing, enhancing or otherwise facilitating spermatogenesis capable of inducing, enhancing or otherwise facilitating spermatogenesis.
                                                                                                                                                                                                                                                                                                           An animal protein as
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                                                                                                                                                                                                                                                                              Disclosure; Page 36;
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RESULT 3
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Best Local Similarity
Matches 579; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (asl) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
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26-OCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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nilarity 99.5%;
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Pred. No. 2e-134;
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ABZ35729 standard; DNA; 582 ВP

(first entry)

Human bcl-w polynucleotide SEQ ID ö 37.

Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.

Homo sapiens.

DE10100588-A1

09-JAN-2001; 2001DE-01000588

09-JAN-2001; 2001DE-01000588

(RIBO-) RIBOPHARMA AG

Limmer ູດ ß Hadwiger

2002-683450/74.

Inhibiting expression of t by introducing into cells to the target. target genes, useful s two double-stranded e.g. for treating tumors, that are complementary

13; Page 30-31; 100pp; German.

RESULT 4
RESULT 4
AREASTOPE
ID AREASTOPE
ID AREASTOPE
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AC AREASTOP The invention relates to inhibiting expression of a target gene in a by introducing at least two oligoribonuclectides (dsnNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleous pairs. At least part of one strand (S1, S2) of the ds structures in each dsnNAI and II are complementary to regions in the target gene. The nucleotide each

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                                 This invention describes a novel method for inhibiting expression of a CC target gene by introducing into the cell that contains the target gene at CC least one oligoribonucleotide (dsnNAI) that has a double-stranded (ds) Structure of not more than 49 consecutive nucleotides (nt), where at CC least a segment of one strand of the ds structure is complementary with CC the target gene and the cells are treated with interferon before introduction of dsnNAI. The method is used to inhibit expression of CC target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, developmental or prion genes, or inhibit expressed in CC pathogenic organisms (particularly plasmodia) or in viruses or viroids CC (pathogenic in humans, animals or plants). Treating the cells with CC interferon greatly increases the extent to which dsnNA can inhibit CC expression of the target genes, and the effect is even greater when dsnNA CC gene fragments used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 35-36; 98pp; German.
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Ś Matches Query Match Best Local S Sequence 582 579; Similarity Conservative BP; 104 A; 156 C; 211 G; 111 T; 0 U; 99.0%; 0 Score 577.2; DB Pred. No. 2e-134; 0; Mismatches u ۲ 9 Length Indels 0 Gaps 0

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Matches 579
                                                                                                                                                                                                 The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonuclectide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytchine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration
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                                                                                                                                                                          Sequence
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ilarity 99.5%;
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03-APR-2003 ABT16642; ABT16642 standard; (first DNA; entry) 3542 ВP

Anti-tumour; DNAzyme; bcl-2 gene; tumour; malignant; chemotherapy; radiation therapy; catalytic domain; enzyme; human; ds.

Homo sapiens

Human bcl-2

gene SEQ ID No

WO200299090-A1

07-JUN-2002; 2002WO-AU000739

07-JUN-2001; 2001AU-00005527

(JOHJ )

JOHNSON & JOHNSON RES

ALd LTD.

Ļ 핂, Saravolac EG, Dass

WPI; 2003-140617/13.

Novel DNAzyme useful for treating tumors, and for enhancing the sensitivity of malignant or virus infected cells to therapy, concatalytic domain and binding domain contiguous to the catalytic domain.

Disclosure; Page 44-45; 67pp; English

The invention relates to a DNAzyme which specifically cleaves mRNA transcribed from a member of the bol-2 gene family. The DNAzymes compi a catalytic domain, binding domains contiguous with the 5° and 3° end the catalytic domain, and therefore hybridise with, the two regions immediately flanking the purine residue of the cleavage site within the composition of the cleavage site within the state of the cleavage site within the state of the cleavage site within the composition of the composition of the cleavage site within the composition of the compositio comprise end of the

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                                                      Spermatogenesis; animal model; ss
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                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA
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                                                                     bc1-3
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                                                                                                                           entry)
                                                                   gene;
                                                                                                                                                                                  581
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                                                                                                                                                                                 ВP
                                                                      Bcl-2;
                                                                      human;
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                                                                      fertility;
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<u>AGTGGGGGCTGGGGGGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG</u>

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CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA

GTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA

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CAGGTCTCCGACGAACTTTTTCAAGGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT

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                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the human bol-w gene encoding Bcl-w protein (see CC AAY05530), a pro-survival member of the Bcl-2 family which is widely compressed and which is essential for spermatogenesis. The invention CC relates generally to a method of treatment and to an animal model for the cidentification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the CC treatment of infertility, or for reducing fertility, by modulating CC spermatogenesis. An animal model carries a mutation is at least one CC allele of the human or murine bol-w gene or in a gene associated with bol C. w. Such animals have disorganised seminferous tubules and are CC substantially infertile, but possess no other major abnormalities as CC determined by histological examination. They can be used to screen for CC therapeutic molecules including genetic sequences capable of inducing, CC cenhancing or otherwise facilitating spermatogenesis in animals, or which CC can induce infertility
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 U; 0 Other:
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DB; AAY05530.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al model exhibiting associated with Bcl
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                                              CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACCC
                                                                                                                                                            AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                    ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
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                                                                                                                                   AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
      TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                                                                           Conservative
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99.1%;
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                                                                                                                                                                                                                                                                                                        Score 573; DB 2;
Pred. No. 2.3e-133;
0; Mismatches 5;
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RESULT 9
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                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                    family, components in the cell death pathway. The bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g.
                                                                                                                                                                                                                                                                                                     Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Column 15/16; 27pp; English.
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DB; AAW61392.
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                            ATGGCGACCCCAGCCTCGGCCCCAGACACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT
                                                                                                   ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT
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/note= "No at-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0012201P
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                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                  Score 567.8; DB 2;
Pred. No. 4.5e-132;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.4%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; 154 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 567.8; DB 2;
Pred. No. 4.5e-132;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 111 T; 0 U; 0 Other;
                                          579
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AXU

ADB52996

standard;

DNA; 582

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ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT

Query Match Best Local S Matches 548

Similarity

90.5%;

Conservative

<u>,,</u>

34;

0;

Gaps

Score 527.6; Pred. No. 5e-10; Mismatches

527.6; DB No. 5e-122;

9;

Length Indels

Local Sin hes 548;

Sequence

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10-APR-2002;
11-APR-2002;
19-APR-2002;
19-APR-2002;
2-APR-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
                                                 The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for
                                                                                                                                                                                                                                                                                                                                                                             Mendrick D,
Elashoff M;
                                                                                                                                                                                                                                                                        Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primary rat hepatocyte toxicity modelling related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening;
                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-731472/69.
                   screening. The present sequence represents modelling related gene sequence
                                                                                                                                                                                                                                               44; SEQ ID NO 3538; 874pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat hepatocyte toxicity modelling; gene; ds
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582
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2002US-0394230P.
2002US-0394253P.
2002US-0407668P.
2002US-0442900P.
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; 2002US-0378370P.
; 2002US-0378652P.
; 2002US-0378653P.
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2002US-0373602P.
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BP; 111
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2002US-0371413P.
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                            The present sequence represents a primary ing related gene sequence from the present
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A; 157
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 G; 114 T; 0 U; 0 Other;
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                                            rat hepatocyte
                                invention.
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RESULT 12
AAV28333
ID AAV28
XX AAV28
XX AAV28
XX CAAT COCO
DE Rat L
XX SS; L
XX SS; L
XX SS; L
XX CAT
COS
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                                                   Guastella
                                                                                                                  23-FEB-1996;
                                                                                                                                                  11-FEB-1997;
                                                                                                                                                                                  04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                  Rattus
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1998-446079/38.
DB; AAW61391.
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                                                                                   COCENSYS
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                                                                                                                                                                                                                                                                                                                                                                                   bc1-2;
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                                                                                                                  96US-0012201P
                                                                                                                                                  97US-00798897
                                                                                 INC
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .579
                                                                                                                                                                                                                                           /product= "bcl-y"
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                   cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA;
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RESULT 13
AAX15945
ID AAX15
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AC AAX15
AC AAX15
XX
DI 20-MA
XX
DE CDNA
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Best Local Similarity
Matches 544; Conserv
                                                                                                                  AAX15945
                                                 20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 579 BP; 111 A; 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Column 13/14; 27pp; English.
               encoding
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                                                                                                                  standard;
                                                                                                                                                                                                  GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG
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                                             (first entry)
                 the
                 rat bcl-y
                                                                                                                  cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%;
                                                                                                                  579
                 protein
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Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g.

The mammalian bol-y genes encode a protein that is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity bol-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell

C; 198 G; 113 T; 0 U; 0 Other;

Score 523; DB Pred. No. 7e-1:0; Mismatches 523; DB 2; No. 7e-121; 2 35; Length 579 Indels 0 Gaps 0

GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAG CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTGGCACTG GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA CTCTTTGGGGCTGCACTGTGTGCTGAGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCCTGGAGGAGGCACGG AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGAGGCGCGG CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC CAGGTTTCCGACGACTTTTCCAAGGGGGCCCCAACTGGGGGCCGTCTTGTGGCATTCTTT CAGGTCTCCGACGAACTTTTTCAAGGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATTAGAGTTCGAGACCCGCTTCCGGCGCACC AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGAGGGCCCAGCAGCTGAC ATGGCGACCCCAGCCTCAACCCCAGACACACGGCTCTAGTGGCTGACTTTGTAGGCTAT ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 579 240 540 540 360 300 300 180 180 120 120 60 480 480 420 420 360 240

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                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes rat bol-y protein (Rbol-y). The constitution also describes human bol-y protein (Hbol-y). Rbol-y and CC specification also describes human bol-y protein (Hbol-y). Rbol-y and CP programmed cell death (apoptosis and necrosis). Rbol-y and Hbol-y conditions associated with a disruption of CP proteins may be used to treat conditions associated with a disruption of CP conditions associated with a disruption of CP conditions associated with a disruption of CP conditions with a subject as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, CP conditions where celerosis, myocardial infarction, vitally induced CP cell death, aging, spinal cord injuries and amystrophic lateral sclerosis CP conditions where cells under go premature cell death as a result of CP conditions where cells under go premature cell death as a result of CP conditions which may on the apparent. They may also be used in this CP condition are contrast, if they act as cell death stimulators, Rbol-y and CP period. In contrast, if they act as cell death stimulators, Rbol-y and CP life span such as cancer (especially kaposi's sarcoma and lung cancer) cand auto/hyperimmune diseases. They may also be used to cause cell death conditions associated with prolonged cell can, and hence control, parasites
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Matches 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 13-16; 26pp; English
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                                                                                       | CCGCTGCACCCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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RESULT 14
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The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY0531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl which animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing,
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Best Local Similarity
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Best Local Similarity
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Q7TS60;
01-OCT-2003
01-OCT-2003
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SMART; SM
PROSITE;
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PROSITE;
SEQUENCE
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STRAIN-Sprague-Dawley;
MEDLINE-22672518; PubMed=12787069;
Itoh T., Itoh A., Pleasure D.;
"Bcl-2-related protein family gene differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation.";
J. Neurochem. 85:1500-1512(2003).
EMBL; AY185100; AA064470.1; -.
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Mammalia; Eutheria; Rodentia;
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SM00265; BH4;
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; PS01080; BH1; 1.

; PS01258; BH2; 1.

; PS01260; BH4 1; 1.

; PS50063; BH4 2; 1.

; PS50063; BH4 2; 1.

; PS50063; BH4 2; 1.
                                        GALVIVGAFFASK 193
                                                                                                                                    QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                           FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                         MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                                                       QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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  GALVTVGAFFASK
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nilarity 98.4%;
Conservative
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219
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Last annotation update)
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Pred. No. 1.4e-80;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                        Score 996; DB 11;
Pred. No. 1.7e-80;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36D6742F4529AFB4
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; Murinae; Rat
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Best Local S
Matches 184
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SMART; SM00265; BH4; 1.

PROSITE; PS50062; BCL2: F

PROSITE; PS01080; BH1; 1

PROSITE; PS01258; BH2; 1
                              Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                    Q9CYW5
Q9CYW5;
01-JUN-2001 (
01-JUN-2001 (
01-JUN-2003 (
Bcl2-like 2.
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Q8CGL4;
01-MAR-2003
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Bcl2-like protein 2.
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MGD; MGI:108052; Bcl212.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                             BCL2L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
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InterPro; IPR003093; Bc12_BH4.
InterPro; IPR003475; BC12_family.
DEFAR. BE0018F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Extraction from neonatal mouse skin after IGF-1 stimulation.", Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL; TISSUE=Skin;
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84; Conservative
                                                                                                                                                                                                                       GALVTVGAFFASK 193
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                                                                                                                                              PRELIMINARY;
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                                             Chordata;
Rodentia;
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Last annotation update)
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Pred. No. 5.1e-77;
                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Airakawa T., Hara A., Fukunishi Y.,
RA Airawa K., Izawa M., Nishi K., Xiyosawa H., Xondo S., Yamanaka I.,
RA Airawa K., Izawa M., Nishi K., Xiyosawa H., Xondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustinche S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wanger J., Kawaji H., Kohtsuki S.,
RA Hyyashizaki Y.,
RETERMINED 
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Best Local Similarity
Matches 143; Conserv
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EMBL; AKO13244; BABZ8740.1; -.

RISSP; Q07817; 1MAZ.

MGD; MGI:108055; Bc1212.

GG; GO:0006315; P:apoptosis; regulator activity; IEA

GG; GO:0006915; P:apoptosis; IEA.

R InterPro; IPR000712; Bc12_BH.

R InterPro; IPR003093; Bc12_BH4.

R InterPro; IPR003093; Bc12_Family.

R Pfam; PF00452; Bc12_Family.

R Pfam; PF00452; Bc12_Family.

R Pfam; PF00452; Bc12_Family: 1.

R Pfam; PF00452; Bc12_Family: 1.

R Pfam; PF00452; Bc12_Family: 1.

R PF0051TE; PS01060; BH4; 1.

R PROSITE; PS01060; BH4; 1.
                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
                                                                                                                                                                                                                            Q8CFR2;
Q8CFR2;
Q1-MAR-2003
01-MAR-2003
01-OCT-2003
SEQUENCE FROM N.A. TISSUE=Eye;
Strausberg R.;
                                                                                                                                                                                                              Bcl2-like
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                                                                                                                  Chordata;
Rodentia;
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95.3%;
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Pred. No. 9.6e-60;
2; Mismatches 5;
                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local :
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InterPro; IPRO03093; Bcl2_EH4.
InterPro; IPRO03093; Bcl2_Em4.
InterPro; IPRO03093; Bcl2_family.
Pfam; PF00452; Bcl2_2; 1.
Pfam; PF002180; BH4; 1.
SMART; SM00365; BCl2_FAMILY; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH4]; 1.
                                                                                                                                                                                                                                                       EMBL; AY005131; AAF88137.1; -.
HSSP; P53563; 1AF3.
G0; G0:0016620; C:membrane; IEA.
G0; G0:0006915; P:apoptosis regulator ac
G0; G0:0006915; P:apoptosis; IEA.
InterPro; IPR000712; BC12_BH4.
InterPro; IPR003095; BC12_BH4.
InterPro; IPR003095; BC12_Family.
InterPro; IPR004725; BC12_reg.
Pfam; PF00452; BC12_reg.
Pfam; PF00452; BC12_reg.
                            PROSITE, PS50062; BCL2 FAMILY; 1
PROSITE, PS01080; BH1; 1.
PROSITE, PS01258; BH2; 1.
PROSITE, PS01259; BH3; 1.
PROSITE, PS01259; BH4 1; 1.
PROSITE; PS0063; BH4 1; 1.
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01-OCT-2000
01-JUN-2003
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"Rabbit Bcl-X.";
Submitted (JUL-2000) to the EMBL/GenB
                                                                                                                                                                                SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
TIGRFAMS; TIGR00865; b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MGD; MGI:108052; Bc1212.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
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       EQUENCE
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PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
233 AA; 25986 MW;
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95.3%;
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Pred. No. 9.6e-60;
2; Mismatches 5
       12F0F30344D53F93 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             activity;
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Best Local Similarity
Matches 94; Conserv
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator ac
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR000712; Bc12_BH.
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR003093; Bc12_FBH4.
InterPro; IPR003475; BC12_reg.
InterPro; IPR00475; BC12_reg.
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EMBL; U51278; AAC53459.1; -...
HSSP; P53563; 1AF3.
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O35844;
O1-JAN-1998
O1-JAN-1998
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PROSITE; PS50062; BCL2; FAMILY;
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
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Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RALVADEVGYKLROKGYVC-----
                                             RALVADFVGYKLRQKGY----
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RELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                     BH4_1; 1.
BH4_2; 1.
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Rodentia;
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41.8%;
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42.0%;
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Last annotation updat
                                                                                        Score 435.5;
Pred. No. 1.1e
22; Mismatches
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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ches 56;
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/ Murinae; Mus
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Best Local S
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PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1
PROSITE; PS50063; BH4_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00452; BC1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
TIGRFRMS; TIGR00865; bC
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01-JUN-2002 (TrE
01-JUN-2002 (TrE
01-JUN-2003 (TrE
Bcl-xl protein.
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Nagafuchi S., Sano J., Kano R., Hasegawa A.;
"Moleculer cloning of feline Bcl-2 family.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ da
EMBL, AB080951; BAB65856.2; --
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator activity;
GO; GO:0006915; F:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR0009712; Bcl2_BH.
InterPro; IPR000903; Bcl2_BH4.
InterPro; IPR002475; Bcl2_family.
InterPro; IPR004775; Bcl2_reg.
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[1]
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Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
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97; Conserv
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PS50063; BH4_2; 1.
233 AA; 26017 MW;
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                                                                                                                                                                                                                                              CGAGEGEGEAD-----PLHQAMRAAGDEFETRERRTESDLAAQLHVTEGSAQQRET
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                                                                                                                                                        QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                                                                                                                                                                                                                  RELVVDFLSYKLSOKGYSWSRFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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                          NGGWDTFVELYGNNAAAESRK---
                                                                SGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                             QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE
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(TrEMBLrel.
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41.6%;
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_FAMILY;
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                                                                                                                                                                                                                                                                                                                                                                                        Score 433.5;
Pred. No. 1.6e
23; Mismatches
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                       -GQERSNRWFLTGMTVAG-VVLLGSLFSRK 233
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Best Local S
Matches 94
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Q9MZS7;
01-OCT-2000
01-OCT-2000
01-JUN-2003
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Q9N1A2;
01-OCT-2000
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                                     Bcl-x long
   Eukaryota;
                    Ovis aries
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Mammalia; Eutheria;
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Lee T.L., Can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                         SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                             QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                       NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                     NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                           CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                             RELVVDFLSYKLSOKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
 g protein.
g (Sheep).
Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEC-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canty J.M.;
                                                    (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TremBlrel. 15, Createu, (TremBlrel. 15, Last sequence up/ (TremBlrel. 24, Last annotation of regulator Bcl-xL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%;
llarity 41.8%;
Conservative 2
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                      15,
24,
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                                                      Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 431.5;
Pred. No. 2.4e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
   Craniata;
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2FA312818B25E17D CRC64;
                                                      sequence up
                                                                                                                                233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity;
   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4e-30;
es 57;
                                                                                                                              ζ
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                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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   Euteleostomi;
                                                                                                                                                                                                                                                           183
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RESULT 11
Q8BQK4
ID 08B0K
AC 08B0K
AC 08B0K
DT 01-MA
DT 01-OC
B-cel
GN B-cel
GN Muser
OC Eukar
OC Mamma
OX NCBI-
RN [1]
RR SEQUE
RC STRAI
RX MEDLI
RA The F
RA the F
RA the F
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Best Local S
Matches 91
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Pfam; PF00452; BC1-2; 1.

SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGREAMS; TIGR00865; bC1-2; 1.

PROSITE; PS01062; BC12; PANILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01256; BH2; 1.

PROSITE; PS01256; BH3; 1.

PROSITE; PS01256; BH4; 1.

PROSITE; PS01260; BH4; 1.

PROSITE; PS01260; BH4; 1.

R PROSITE; PS01260; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Ovary;

Mirray J.F., Dong Y.B., Leigh
Mirray in the sheep ovary.";

Submitted (JUL-1999) to the EI
EMBL; AF164517; AAF89532.1;

HSSP; E53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator ac
GO; GO:0016319; P:apoptosis; IEA.
InterPro; IPR000712; BC12_BH.
InterPro; IPR003099; BC12_Family.
InterPro; IPR002475; BC12_family.
InterPro; IPR00472; BC12_reg.
                                                                                                                                                                              Q8BQK4
Q8BQK4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
                                       STRAIN=C57BL/6J; TISSUE=Body; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                888
                                                                           SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=10090;
                                                                                                                  Eukaryota;
Mammalia;
                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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                                                                                                                                                                   leukemia/lymphoma
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                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                        GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
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                                                                                                                                                                                                                                                                                                                                                                                                  NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                         D-----PLHQAMRAAGDEFETRERETESDLAAQLHVTPGSAQQRETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caprinae;
                                                                                                                                                                3 (TrEMBLrel. 23, 0
3 (TrEMBLrel. 23, 1
3 (TrEMBLrel. 25, )
kemia/lymphoma 2.
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                          (Mouse)
                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                              Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 428.5; DB b;
Pred. No. 4.5e-30;
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                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                               sequence update) annotation updat
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                         Group
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             8
                          Phase
                                                                                                                                                                               update)
             hase I & II
| functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pecora;
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                                                                                                                                                                                                                                                                                                229
             annotation
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Q7TSNA
ID Q7TSN
AC Q7TSN
AC Q7TSN
AC Q7TSN
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
Rattu
OC Eukar
OC Mamma
OC NCBI
RN [1]
RN [1]
RN [1]
RN [1]
RN EMBL;
SQ SEQUE
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Best Local S
Matches 87
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Best Local S
Matches 87
                                                                                        STRAIN-Wistar;
Tanaka T., Nangaku M.;
"Rat Bc12-like protein.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF512835; AAP47159.1; -.
SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000712; Bcl2_BH.
InterPro; IPR003093; Bcl2_BH4.
InterPro; IPR002475; BcL2_family.
InterPro; IPR004725; Bcl2_reg.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF00152; Bcl-2; 1.
                                                                                                                                                                                                                         Bcl2-like protein.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                  Q7TSN8;
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005829; C:cytosol; IDA.
GO; GO:0008189; F:apoptosis inhibitor activity;
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006915; P:apoptosis; IDA.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Q7TSN8
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                                                                                                                                                                                                                                                                                                                                                                                   142
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                                              . Similarity
87; Conser
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87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSFLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                           GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                               GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLRPLVATTGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTRALVADEVGYKLROKGYVCGAG------PG-----PG------
DNREIVMKYIHYKLSORGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHRDMAART
                       DTRALVADFVGYKLRQKGYVCGAG------PG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHRDMAART
                                              Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                        41.0%;
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37.5%;
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                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          Created)
                                            Score 413; DB 11;
Pred. No. 1.1e-28;
4; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 413; DB 11;
Pred. No. 1.1e-28;
                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B726BFFA3AA1C718 CRC64;
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                                                                   Length 236;
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                                              Indels
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                                                                                                                                                                                                                                                                                                                                               RX MEDLINE-22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wiskin R.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villaion D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,

RA Jones S. T. Mayra W A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001
01-JUN-2003
Bcl-XL-like
GO; GO:0016329; F:apoptosis regulator GO; GO:0006915; P:apoptosis; IEA. InterPro; IPR0030912; Bc12_BH4. InterPro; IPR003093; Bc12_BH4. InterPro; IPR003475; Bc12_family. Pfam; PF00452; Bc1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21299061; PubMed=11406282;

Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong Choning and characterization of zfBLP1, a Bcl-XL zebrafish, Danio rerio(1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ev
Actinopterygii, Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                           Submitted
                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2L OR BLP1
                                                                                                                       ZFIN;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Body;
                                                                                                                                                                                                                                                                            Proc.
                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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                                                                                                                 AF317837; AAK81706.1; -.
BC044130; AAH44130.1; -.
ZDB-GENE-010730-1; bc121
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                                                                                                                                                                             (JAN-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 24, Last annotation
protein 1 (Bol21 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EGPAADP----LHQAMRAAGDEFETRERRTFSDLAAQLHVTPGSAQQRFTQ
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ta; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
                                                                                                activity;
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RESULT 15

Q9BDD5 PRELIMINARY; PRT; 180 AA.

AC Q9BDD5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLREL. 24, Last annotation update)
DE Anti-apoptotic regulator Bcl-xL (Fragment).
OS Bos taurus (Bovine).
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Best Local S
Matches 77
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Best Local Similarity 36.6
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
ICh T., Itch A., Pleasure D.;
"Bcl-2-related protein family gene ey
differentiation.";
J. Neurochem. 85:1500-1512(2003).
EMBL, AY185099; AAO64469.1; -.
SEQUENCE 79 AA; 8602 MW; 47EDFB31
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SMART; SM00337; BCL1; 1-
PROSITE; PS50062; BCL2; PAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS50063; BH4 2; 1.
SEQUENCE 238 AA; 26253 MW; (
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01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                         MEPLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVL
                                                                                                                                                                                                                                                                                                                                                                                                       MEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVL
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                                                                                                                                                                                                                                                                          TGAVALGALVTVGAFFASK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%;
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1; Mismatches
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47EDFB3EE2909485 CRC64;
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    AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR

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Matches 76
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"Characterization of the bovine bcl-xL gene and related Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP245488; AAX31307.1; -
EMBL; AP245489; AAX31308.1; -.
HSSP, Q07817; 1MAZ.
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SEQUENCE
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                                                                                                                                                                                                                                                             Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                             GO; GO:0016329; F:apoptosis regulator GO; GO:0006915; P:apoptosis; IEA. InterPro; IPR002475; BC12 Family. InterPro; IPR002475; BC12 Family.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                           PROSITE;
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Mammalia; Eutheria; Cetartiodactyla;
158
                     164
                                                     98
                                                                                      38
                                                                                                            44
                                                                                                                                    76;
                                                                                                                                             Similarity
                                                                                                                                                                                                              PS50062; BCL2 FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                  E--GNWASVRTVLTGAVALGAL
                                           GALCVESVDKEMQVLVGRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ 157
                                                                                     QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
                                                                                                       QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG
ERFNRWFLTGMTVAGVVLLGSL
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180 AA;
                                                                                                                                    Conservative
                                                                                                                                                                                            180
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                                                                                                                                            Score 401; DB 6
Pred. No. 9e-28;
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actyla; Ruminantia; Pecora;
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179
                     183
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                    activity;
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                                                                                                                                 45;
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                                                                                                                                 2
                                                                                                                                 Gaps
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                                                                                      97
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Search completed: March 25, 2004, 15:44:26 Job time : 37 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1007
1 MATPASAPDTRALVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March 25, 2004, 15:19:05; Search time 10 Seconds (without alignments) 1004.954 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length DB
     BCLW MOUSE
ARI XENLA
BCLX CHICK
GECLX HUMAN
BCLX HUMAN
BCLX HOUSE
BCLZ CHICK
BCL2 CHICK
BCL2 CHICK
BCL2 CHICK
BCL2 CHICK
BCL2 HUMAN
BCL2 HUMAN
BCL4 HUMAN
BAXA HUMAN
BCLB HUMAN
BFLI HUMAN
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  Description
8 homo sapien
6 homo sapien
0 homo sapien
0 mus musculu
9 african swi
5 african swi
                                                                                                                                              2 homo sapien
8 caenorhabdi
3 bos taurus
4 homo sapien
3 coturnix co
9 homo sapien
7 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                      7 xenopus lae
6 gallus gall
7 sus scrofa
7 homo sapien
3 mus musculu
3 rattus norv
9 gallus gall
8 bos taurus
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4. U	44	43	42	41	40	39	38	37	36	អូ	34
79	79	79.5	79.5	80	82.5	82.5	83.5	85	85.5	87	98.5
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541	396	872	872	541	3432	1440	660	275	358	3433	179
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FTCD_RAT	PORA PYRFU	SYA STRR6	SYA STRPN	FTCD MOUSE	POLG_JAEVJ	POLG JAEVN	SQHC_BRAJA	DAPB_AGRT5	GLNA LACSA	POLG KUNJM	EAR_ASFE4
088618 r		Q8dpc7 st		Q91xd4 m	P32886 j	P14403 j		Q8uiv8 ag		P14335 k	Q07818 african swi
r formimide	Yrococ	streptococc	streptococc	m formimido	genome	genome	bradyrhizok	grobact	lactuca sat	genome	frican

## ALIGNMENTS

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DNA Res. 3:321-329(1996).  [3]  SEQUENCE FROM N.A.  TISSUE=Lung;  MEDLINE=22388257; PubMed=12477932;  MEDLINE=2238257; Medle N.K., Schaler C.M., Schaler C.M.,	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE=96358615; PubMed=8761287;  Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,  Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;  "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  Oncogene 13:665-675(1996).  [2]  SEQUENCE FROM N.A.  TISSUE=Brain;  MEDLINE=97191544; PubMed=9039502;  MEDLINE=97191544; PubMed=9039502;  MEDLINE=97191544, Seki N., Ishikawa KI., Ohira M., Kawarabayasi Y.,  Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  "Prediction of the coding sequences of unidentified human genes. VI.  The coding sequences of 80 new genes (KIAA0201 KIAA0280) deduced by	HUMAN STANDARD; PRT; 193 AA.  92843; 01.NOV-1997 (Rel. 35, Created) 01.NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 15-MS regulator Bcl-W (Bcl-2-like 2 protein).  Apoptosis regulator Bcl-W (Bcl-2-like 2 protein). BCL2L2 OR BCLW OR KIAA0271.  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;

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RESULT
BCLW MC
ID BC
AC P7
DT 01
DT 01
DT 15
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Matches 193
W_MOUSE
BCLW_MOUSE
P70345;
01-NOV-1997
01-NOV-1997
15-MAR-2004
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SMART; SM00265; BH4; 1.

PROSITE; PS50062; BCL2 FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS50063; BH4 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis.
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0008199; F:apoptosis inhibitor activity; GO; GO:0006916; P:anti-apoptosis; TAS. GO; GO:0007283; P:spermatogenesis; TAS. InterPro; IPR000712; Bc12_BH.
InterPro; IPR00099; Bc12_BH4.
InterPro; IPR0002475; BC12_Family.
Pfam; PF00482; Bc1-2; 1.
Pfam; PF00180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D87461; BAA19666.1
EMBL; BC021198; AAH21198
HSSP; Q07817; IMAZ.
Genew; HGNC:995; BCL2L2.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U59747; AAB09055.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 Bcl-2 homology 1 SIMILARITY: Contains 1 Bcl-2 homology 2 SIMILARITY: Contains 1 Bcl-2 homology 4 SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in a wide range of tissues, and salivary gland.
DOMAIN: BH4 domain seems to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601931;
                                                                                                                         181
                                                                                                                                                 181
                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                  193;
                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                      GALVTVGAFFASK 193
                                                                                                                                                                                                  QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                               MATPASAPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT
                                                                                                                         GALVÍVGÁFFÁSK 193
                                                                                                                                                                          QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                85
136
193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFICITY: Expressed in ide range of tissues, with
                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0;
    (Rel. 35, Created)
(Rel. 35, Last seq
(Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                    ΑΑ,
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH21198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   29 BI
104 BI
151 BI
20774 MW;
     sequence up
                                                                                                                                                                                                                                                                                                                                                                                   BH4.
BH1.
BH2.
3792243A50281761 (
                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                  Score 1007;
Pred. No. 1.1
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be involved
                 update)
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highest levels in b
                                                        193
                                                        Ą
                                                                                                                                                                                                                                                                                                                                                .1e-83;
                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (BH1) domain.
2 (BH2) domain.
4 (BH4) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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(BH2)
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                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell lines
                                                                                                                                                                                                                                                                                                                                                            193;
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                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                          Query Match
Best Local :
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InterPro; IPR003093; Bc12_BH4.
InterPro; IPR002475; BCL2_family.
InterPro; IPR002475; BCL2_family.
Pfam; PP00452; Bc1-2; 1.
Pfam; PP02180; BH4; 1.
SMART; SM00337; BCL; 1.
SWART; SM00337; BCL; 1.
                                                                                                                                                                                                           PROSITE; PS50062; BCL2_FAM:
PROSITE; PS01080; BH1; 1.
PROSITE; PS01280; BH2; 1.
PROSITE; PS01260; BH4 1; 1
PROSITE; PS50063; BH4_2; 1
                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Russell L.D., Macgregor G.R.; "Testicular degeneration in Bclw-deficient mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/10J;
MEDLINE=98150183; PubMed=9500547;
ROSS A.J., Waymire K.G., Moss J.E., Parlow A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.

MEDLINE=96358615; PubMed=8761287;

Gibson L., Holmgreen S.P., Huang D.C., Berna Jenkins N.A., Sutherland G.R., Baker E., Add "bcl-w, a novel member of the bcl-2 family,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N
                                                                                                                                                              DOMAIN
                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 13:665-675(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis regulator
BCL2L2 OR BCLW.
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                    Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:108052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 1 Bcl-2 homology 1 SIMILARITY: Contains 1 Bcl-2 homology 9 SIMILARITY: Contains 1 Bcl-2 homology 4 SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Expressed in almost all myeloid
in a wide range of tissues, with highest levels in b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and salivary gland.

DOMAIN: BH4 domain seems to be involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Genet. 18:251-256(1998). FUNCTION: Promotes cell survival
                                                                                                                                                                                                                                                                                                                                                                                                U59746; AAB09056.1; -. AF030769; AAB86430.1; -.
                  <u>გ</u>
                                                                                                           Similarity
    FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                           MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT
                                            MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                           9
85
136
193
                                                                                            99.3%;
nilarity 99.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse)
                                                                                                                                                 AA,
                                                                                                                                                                                                                                                                                                                                                                         Bc1212
                                                                                                                                               29
104
151
20790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-W (Bcl-2-like 2 protein)
                                                                                                                                                                                                                                                                   FAMILY; 1.
                                                                                            Pred.
1; Mis
                                                                                                           Score 1000;
Pred. No. 4.
                                                                                                                                               BH2.
36CA185F5945DFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bernard O., C
                                                                                          1.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no rest
                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BH1)
(BH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promotes cell survival.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BH4)
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domain. domain. domain.

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restrictions on tent is in no and

EMBL outstation

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collaboration

anti-apoptotic

in brain,

colon,

cell lines and

Skinner

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Copeland L., Cory S.

N.G.,

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Length

193;

Indels

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Gaps

120 60 60

В Ś

121 121

QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEBARRLREGNWASVRTVLTGAVAL 180 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL

180 120

61

FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG

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                           Query Match
Best Local S
Matches 125
                                                                             TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XENLA
                                                                                                                  Apoptosis;
NON_TER
DOMAIN
                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                    Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, characterization and expression cell-survival genes.",
Gene 158:171-179(1995).
-!- FUNCTION: Could be the homolog of mamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis regulator R1 (XR1) (Fragment).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR1 XENLA
Q91827;
                                                                                                      DOMAIN
                                                                                                                                                       PROSITE; PS50062; BCL2_FAMILY;
                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cruz-Reyes J., Tata J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last 15-MAR-2004 (Rel. 43, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95331613;    PubMed=7607538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: Developmental regulation only occurs in the brain of mid-metamorphosic to post-metamorphosic tadpoles and adults, where an increase of several fold has been observed. SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain. SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain. SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
                            125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                     Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                X82462; CAA57845.1; -.
  10
                                      Similarity
                                                                                                                                                                   PS01080; BH1; 1.
PS01258; BH2; 1.
TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALVTVGAFFASK 193
                                                                                                                                                                                                                                          IPR000712; Bcl2_BH.
IPR003093; Bcl2_BH4.
IPR002475; BCL2_family.
                                                                            120
171
207
228 ;
                                                                                                                                           Transmembrane.
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                 139
                                                                            186
227
25068
                                   64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e homolog of mammalian Bcl-W. Membrane-bound (Potential)
                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
                       Pred. No. 3.8e
L; Mismatches
                                    Score 646.5;
Pred. No. 3.0
                                                                         POTENTIAL.
C499D449A585F8A9 CRC64;
                                                                                                                 BH1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                       3.8e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of two Xenopus bcl-2-like
                                                  DB 1;
                                                Length
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01-FEB-1995 (Rel. 31, Created)

10-NOV-1997 (Rel. 35, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).

BCLZLI OR BCLX OR BCL-X.

BCLZLI OR BCLX OR BCLX.

BCLZLI OR BCLX.

BCLZLI OR BCLX OR BCLX.

BCLZLI OR BCLX.

BCLXLI OR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vilagrasa X., Mezquita C., Mezquita J.;
"Differential expression of bol-2 and bol-x during chicke spermatogenesis."
Mol. Reprod. Dev. 47:26-29(1997).
-!- FUNCTION: Dominant regulator of apoptotic cell death.-form displays cell death repressor activity, whereas isoform promotes apoptosis (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial membranes and per
                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boise L.H., Gonzalez-Garcia M., Postema C.E., I
Turka L.A., Mao X., Nunez G., Thompson C.B.,
"bcl-x, a bcl-2-related gene that functions as
of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97264485; PubMed=9110311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Hubbard White Mountain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM SHORT). MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                         apoptotic activity (By similarity).
SIMILARITY: Contains 1 Bc1-2 homology 1
SIMILARITY: Contains 1 Bc1-2 homology 2
SIMILARITY: Contains 1 Bc1-2 homology 3
SIMILARITY: Contains 1 Bc1-2 homology 4
SIMILARITY: Belongs to the Bc1-2 family.
                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Highest expression in organs with lymphoid
                                                                                                                                                                                                                                                                                                                        DOMAIN:
                                                                                                                                                                                                                                                                                            function. Intact
                                                                                                                                                                                                                                                                                                                                             development
                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          envelope (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
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                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q07816-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q07816-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
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                                                                                                                                                                                                                                                                                                                        BH4 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    =
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                               BHI
                                                                                                                                                                                                                                                                                                                                                                                             Sequence=VSP_000514;
                                                                                                                                                                                                                                                                                                                   seems to be involved in the anti-apoptotic
                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                               BH2 domains are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Postema_C.E., Ding L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bcl-x during chicken
                                                                                                                                                                       (BH1)
(BH2)
(BH3)
(BH4)
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Matches 95
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SMARR; SM00365; BH4; 1.
TIGREAMS; TIGRO0865; bCl2-2; 1.
PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01286; BH2; 1.
PROSITE; PS01286; BH2; 1.
PROSITE; PS01286; BH3; 1.
PROSITE; PS01260; BH4; 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003093; Bc
InterPro; IPR002475; Bc.
InterPro; IPR0024725; Bcl
Pfam; PF00452; Bcl-2; 1
Pfam; PF02190
                                                                                                                                                       BCLX_PIG
077737;
                                                                                                                                                                            LPIG
SEQUENCE FROM N.A.

MEDIIND=99171363; PubMed=10072723;

Bartling B., Hoffmann J., Holtz J.,

"Quantification of cardioprotective short-term hibernating myocardium.";
                                                                     15-UIL-1999 (Rel. 38, Created)
15-UIL-1999 (Rel. 38, Last sequence update)
15-UIL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
BCL2L1 OR BLC2L OR BCLX.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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DOMAIN
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PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS50063; BH4 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z23110; CAA80657.1; -.
EMBL; U26645; AAB07677.1; -.
PIR; A47537; A47537.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send
                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                     146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                   186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK
                                                                                                                                                                                                                                                                                86
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                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53563; 1AF3
                                                                                                                                                                                                                                                                                                  66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
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                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an
                                                                                                                                                                                                                                                           LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE
                                                                                                                                                                                                                                                                                                                                                             LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                 ------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
                                                                                                                                                                                                                                                                                                                                          RELVIDEVSYKLSORGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/
nn email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
125
126
185
185
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                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                  STANDARD;
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194
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41.7%;
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Bcl2_BH4.
BCL2_family.
Bcl2_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                        BH1.
BH2.
POTENTIAL
POTENTIAL
ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
LSRK -> VRTALP (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                            Score 432.5; DB 1;
Pred. No. 7.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        FTId=VSP_000514.
A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
           schulz R., Heusch G., Darmer D.;
gene expression in porcine
                                                                                                                                                                  233
                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                  62:
                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                        Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                      1 229;
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                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ001203;
   125
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14
                                                                                                                                                                                                                                                                                                                                                                                            Q07817;
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                                                                                                      11
                                                                                                                         94;
                                                                                  σ
                                                                                                                                   Similarity
                     QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                      RALVADEVGYKLRQKGY---
                                                            CGAGPGEGPAAD-----PLHQAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRET
                                                                                  RELVVDFLSYKLSOKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
   QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                          NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                4
129
180
210
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                                                                                                                                                                                                                             Mitochond
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                             1MAZ
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41.8%; 42.9%;

Score 431.5; DB Pred. No. 9e-32; 1; Mismatches

DB 1; 57;

Length Indels

233; 53;

Gaps V----V

28 4.

140

124

80 9 POTENTIAL

18BF6FA0441912B2 CRC64;

21;

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envelope (By similarity).

C: | DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domain is required for both heterodimerizaty. The bH1 and BH2 domains are required for both heterodimerizaty. The other Bc12 family members and for repression of cell dear continuity. The cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has continuity (By similarity).

C: SIMILARITY: Contains 1 Bc1-2 homology 1 (BH1) domain. C: SIMILARITY: Contains 1 Bc1-2 homology 2 (BH2) domain. C: SIMILARITY: Contains 1 Bc1-2 homology 3 (BH3) domain. C: SIMILARITY: Contains 1 Bc1-2 homology 4 (BH4) domain. C: SIMILARITY: Contains 1 Bc1-2 homology 4 (BH4) domain. C: SIMILARITY: Belongs to the Bc1-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0865; bcl-2; 1.

PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01250; BH4_1; 1.

PROSITE; PS50063; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Cell. Cardiol -!- FUNCTION: Potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000712; Bc12_BH.
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR003475; BC12_family.
InterPro; IPR003475; Bc12_reg.
Defort BE00452; Bc12_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) and apoptotic activity is inhibited by association with SIVA isofoli. Inhibits activation of caspases (By similarity). Appears to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cardiol.
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24 B. 100 B. 148 B. 195 B. 195 B. 195 B. 195 B. 196 P. 196
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                                                                                                                                                                                                                                                                                                                                                                          ion;
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RA APPOLINE=93:

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Shevinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smailus D.E.,
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"Generation and initial analysis of more than 15,000 full-length
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korsmeyer S.J.;
"Multiple Bc1-2
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        INTERACTION WITH (
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                                                                                                                                                                  "Bax-independent inhibition
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Turka L.A.,
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MEDLINE=93364977; I
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        SIVA.
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vine B., Boise L
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Muchmore S.W., Sattler M., Liang H., Voon H.S., Nettesheim D., Chang B.S.,
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Sattler M., Liang H., Nettesheim I
Eberstadt M., Yoon H.S., Shuker S.
Thompson C.B., Fesik S.W.;
                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis.";
Science 275:983-986(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiation-induced apoptosis.";
Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND
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                                                                                                  - SIMILARITY: Contains 1 B
- SIMILARITY: Belongs to t
                                                                                                                                                                                      INSUE SPECIFICITY: Bcl-X(S) is expressed at high levels in cells that undergo a high rate of turnover, such as developing lymphocytes. In contrast, Bcl-X(I) is found in tissues containing long-lived postmitotic cells, such as adult brain.

DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.

PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (UDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-X(S) isoform promotes apoptosis.

SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2. Heterodimerization with BAX does not seem to be required for antiapoptotic activity. Isoform Bcl-X(L) binds to Siva isoform 1.

SUBCLIJULAR LOCATION: Mitochondrial membranes and perinuclear
                                      s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative
Name=Bcl-X(L);
IsoId=Q07817-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       envelope (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dulation of cell death bx Bcl-xL through cac. Natl. Acad. Sci. U.S.A. 95:554-559(1998) FUNCTION: Potent inhibitor of cell death.
                                                                                                                                                                                                                                                                                                                                                 Name=Bcl-X(beta);
                                                                                                                                                                               activity
                                                                                                                                                                                                                                                                                                                                                               Name=Bcl-X(S);
IsoId=Q07817-2;
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                                                                                                  1 Bcl-2 homology 1
1 Bcl-2 homology 2
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o the Bcl-2 family.
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Chang B.S.,
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Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BC1; 1.
SMART; SM00337; BC1; 1.
SMART; SM00265; BH4; 1.
ITICRFAMS; TICR00865; bc1-2; 1.
PR05ITE; PS01086; BC12 FAMILY; 1
PR0SITE; PS01080; BH1; 1.
PR0SITE; PS010259; BH3; 1.
PR0SITE; PS010259; BH3; 1.
PR0SITE; PS010259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; B47537; B47537.
PIR; JE0203; JE0203;
PDB; IBXL; 29-CCT-97.
PDB; ILXL; 21-APR-97.
PDB; IMAZ; 21-APR-97.
PDB; IG5M; 21-MAR-01.
PDB; IG5M; 21-MAR-01.
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GO: 0008189;
GO: 0006916;
GO: 0008637;
GO: 0008634;
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Z23115; CAA80661.1;
           29
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; PS50063; BH4_2;
                                                                       Similarity
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        CGAGPGEGPAAD-
                                           RALVADFVGYKLROKGY-----
                         RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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21-APR-97.
21-APR-97.
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13-JUN-01.
                                                                                                                                                                                                                                                                                                                               Mitochond
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148
156
176
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135
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129
180
210
210
                                                               Conservative
                                                                                                                                                     138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:mitochondrion; TAS.
F:appctosis inhibitor activity;
P:anti-appctosis; TAS.
P:appctocic mitochondrial chang
P:negative regulation of surviv
                                                                      42.6%;
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156
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Bcl2_reg.
Alternative
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D->A: NC
D->A: NC
WD->GA:
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CLEAVAGE (
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Pred. No. 1.
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VNW->AIL:
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/FTId=VSP_
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D->A: NO CLEAVAGE
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FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
VGDVDS (in isoform Bcl-X(beta)).
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HETERODIMERIZATION WITH BAX.
EFECT ON CASPASE-1 CLEAVAGE.
EFECT ON CASPASE-1 CLEAVAGE.
REDUCES ANTI-APOPTOTIC ACTIVITY
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survival gene products;
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isoform Bcl-X(S)).
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WA Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
Whata S., Seldin M.F., Nunez G.;
Wolta S., Seldin M.F., Nunez G.;
Genomic organization, promoter region analysis, and chromosome
of che mouse bel-x gene.";

L. Immunol. 158:4750-4757(1997).
C. I-FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) anti-
proportion: activity is inhibited by association with SIVA isoform
of the mouse bel-x (By similarity). Appears to
regulate cell death by blocking the voltage-dependent anion
channel (VDAC) by binding to it and preventing the release of the
caspase activator, cytochrome c, from the mitochondrial membrane.
The Bcl-X(S) isoform promotes apoptosis.
C. ISUBUNIT: Bcl-X(S) isoform promotes apoptosis.
SIBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By
similarity). Heterodimerization with BAX does not seem to be
required for anti-apoptotic activity (By similarity). Isoform Bcl-
cc X(L) binds to Siva isoform 1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6 X CBA; TISSUE=Thym

MEDLINE=98051053; PubMed=9390687;

Yang X.-F., Weber G.F., Cantor H.

"A novel Bcl-x isoform connected of

apoptosis in T cells.";

Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCLX, MOUSE STANDARD; PRT; 233 AA. (264373; Q60657; Q60658; Q61338; Q1.NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Apoptosis regulator Bcl-X (Bcl-2-like 1 protein) BCL2L1 OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95052604; PubMed=7963517; Fang W., Rivard J.J., Mueller D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=95331139; PubMed=7607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97289584; PubMed=9144489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kamesaki H.,
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Sciurognathi; Muridae; Murinae;
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
  DOMAIN
DOMAIN
                                    Apoptosis;
                                                                                                         SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
TIGREPAMS; TIGE00865; bCl-2; 1.
PROSITE; PS50062; BCL2 FAWILY;
PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cleatween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                   Pfam; PF00452; Bcl-2;
Pfam; PF02180; BH4; 1.
                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIM: Proteolytically cleaved by caspases during similarity). The cleaved protein, lacking the BH apoptotic activity (By similarity). SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) dc SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) dc SIMILARITY: Contains 1 Bcl-2 homology 2 (BH3) dc SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) dc SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) dc SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: The BH4 domain is required for anti-apoptotic acti
The BH1 and BH2 domains are required for both heterodimeri
with other Bc12 family members and for repression of cell
                                                                                                                                                                                                                                              MGI:88139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       postnatal
DOMAIN: Th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=064373-4; Sequence=VSP 000519; TISSUE SPECIFICITY: Widely expressed, with highest levels in the brain, thymus, bone marrow, and kidney. Bcl-X(L) and Bcl-X(delta-TM) expression is enhanced in B and T lymphocytes that have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q64373-3; Sec
Name=BCL-X(delta-TM)
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                                                                                              PS01080; BH1;
PS01258; BH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement
                                                                                                                                                                                        IPR000712; Bcl2_BH.
IPR003093; Bcl2_BH4.
IPR003475; BCL2_family.
IPR004725; Bcl2_reg.
                                             PS501260; BH4_1; 1.
PS50063; BH4_2; 1.
; Mitochondrion; Al
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129
180
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                                                Alternative
BH4
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predominantly
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heterodimerization
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Best Local &
Matches 93
SEQUENCE FROM N.H.

SEQUENCE FROM N.H.

STRAIN-Sprague-Dawley; TISSUB-UVL.,

STRAIN-Sprague-Dawley; TISSUB-UVL.,

STRAIN-Sprague-Dawley; TISSUB-UVL.,

MEDLINE-95129487; PubMed-7828536;

Tilly K.I., Kenton M.L., Johnson A.L.;

Tilly M.L., Tilly K.I., Kenton M.L., Johnson A.L.;

Tilly J.L., Tilly K.I., M.L., M.L., Johnson A.L.;

Tilly J.L., Tilly K.I., M.L., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECLX_RAT STANDARD; PRT; 233 AA. P53563; P70613; P70614; Q62678; Q62836; Q64087; Q61-0CT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 34, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Apoptosis regulator Bcl-X (Bcl-2-like 1 protein). BCL2L1 OR BCLX.
                                                                                                                                                                                                                                                                                                                                                    unspliced RNA,
                                                                                                                                                                                                                                                                                                                                                                                     "An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
Wesselingh S.L., David G
Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT
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                                                                                                                                                                                                                                                                                                                                                                                                          Shiraiwa N., Inohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michaelidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96278736; PubMed=8662675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A. (ISOFORMS X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSUE-Brain;
                                                                                                                                                                                                                                                                                                                               Biol.
                                                                                                                                                                                                                                                                                                                                                                                  raiwa N., Inohara N., Okada S. additional form of rat Bcl-x,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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                                                                                                                                                                                                                                                                                                                            Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVSDELFQGGENWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAGFGEGFAAD------PIHQAMRAAGDEFETRFRRTFSDLAAQIHVTFGSAQQRFT
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126
                                                                                                                                                                                                                                                                                                                rorm of rat Bcl-x, Bcl-xbeta, ger promotes apoptosis in promyeloid 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Æ,
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188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>Ω</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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Missing (in
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Pred. No. 1.7e-31;
2; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL-X(beta)).
/FTId=VSP_000518.
LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK-> GHDCGWCGSAGLTLQSEVTRH (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId-VSP 000517.
DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
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/FTId=VSP_000519.
24D2AC79887E072E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND
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                                                                                                                                                                                                                                                                                                                                                                                                          Yuzaki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x(s)).
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                                                                                                                                                                                                                                                                                                                                                                               , Shoji S.-
generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a M., Hardw
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                       cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q64128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hardwick J.M.;
                                                                                       ition of granulosa constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                            d by
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J. Biol.
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bcl-2 and bcl-xlong messenger ribonucleic Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aritomi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channnel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-X(S) and Bcl-X(beta) isoforms promote apoptosis.

SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). Isoform Bcl-X(L) binds to Siva isoform 1 (By similarity).

SUBCELIULAR LOCATION: Mitochondrial membranes and perinuclear
                                                                                                                                                                                                                                                                                                                                                                                                   activity (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 2 SIMILARITY: Contains 1 Bcl-2 homology 2 SIMILARITY: Contains 1 Bcl-2 homology 3 SIMILARITY: Contains 1 Bcl-2 homology 4 SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P53563-3; Sequence=VSP_000521;
TISSUE SPECIFICITY: Expressed in most tissues. Bcl-X(beta) is specifically expressed in cerebellum, heart, and thymus. In the ovary, the predominant form is Bcl-X(L), with a small but detectable level of Bcl-X(S).

DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerizations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     envelope (By similarity).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Potent inhibitor of cell death. Isoform Bcl-X(L) antiapoptotic activity is inhibited by association with SIVA isoform 1. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Bcl-X(beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Bc1-X(S);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bc1-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Bcl-X(L);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P53563-2; Sequence=VSP_000520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P53563-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunishima
             Bcl-2;
BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272:27886-27892 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9346936;
nima N., Inohara N., Ishibashi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing; Named isoforms=3;
                                                    _family.
                                                                                                                                                        ALT_INIT.
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                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                  1 (BH1)
2 (BH2)
3 (BH3)
4 (BH4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid levels.";
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RESULT 9
BCL2\_CHICK
ID BCL2\_CHICK

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                                                                                                                                            Matches
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Best Local
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TIGRPAMB; TIGR00865; BROSITE; PS50062; B
PROSITE; PS01080; B
PROSITE; PS01258; B
PROSITE; PS01259; B
PROSITE; PS01260; B
PROSITE; PS01260; B
PROSITE; PS01260; B
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HELIX
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis;
                           125
185
              141
                                        81
                                                       66
                                                                      29
                                                                                                  11 RALVADFVGYKLRQKGY------V
                                                                                    σ
                                                                                                               Similarity 41.0
93; Conservative
                                                                   CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
             SGGWAEFTALYGDGALEBARRLRE--GNWASVRTVLTGAVALGAL
                           QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEFWIQE
                                       QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                      NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                          185
187
233
                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                         129
129
180
210
126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GR00865; bcl-2;
                                                                                                                                           ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     365; bcl-2; 1.

BCL2 FAMILY;

BH1; 1.

BH2; 1.

BH3; 1.

BH4_1; 1.

BH4_2; 1.
                                                                                                                                                  100
148
195
198
                                                                                                                      42.6%;
                                                                                                                                           26158
                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing; Transmembrane;
                                                                                                               22;
                                                                                                               Score 428.5; DB:
Pred. No. 1.7e-31
2; Mismatches 5
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H - V D (I
                                                                                                                                                                                                                                                                                                                                                                                   BH2.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                         IDYSGDIPGLL (in isoform /FTId=VSP_000521.
                                                                                                                                                                                                                                                                                                                                                       DTFVDLYGNNAAAESRKGQERFNRWFLIGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۳.
                                                                                                                                           2B62B6C63864BC8F CRC64;
                                                                                                                                                                                                                                                                                Id=VSP 000521.

> Q (IN REF. 1).

> S (IN REF. 2).

> E (IN REF. 2).

> L (IN REF. 4).

- SS (IN REF. 4).

- ST (IN REF. 4).

- P (IN REF. 4).
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                                                                                                                             DB 1;
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                                                                                                               Indels
                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                 Bc1-X(beta))
              183
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                                                                                                               53;
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                            184
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or send a
 Pfam;
SMART;
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                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                           This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (ApAF-1).

-!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAX and Bc1-X(I). Heterodimers, and heterodimers intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with ApAF-1 and RAF-1 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen, kidney, heart, ovary and brain, with the highest levels in the thomas of the machine highly levels appread in all tigning with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993
01-APR-1993
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_
                                 Pfam;
                                      InterPro; IPR000712; Bcl2 BH.
InterPro; IPR003093; Bcl2 BH4.
InterPro; IPR002475; BcL2 family.
InterPro; IPR0024725; Bcl2 reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eguchi Y., Ewert D.L., Tsujimoto Y., "Isolation and characterization of the chicken in a variety of tissues including lymphoid and adult and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cazals-Hatem D.L., Louie D.C., Tanaka S., Rec
"Molecular cloning and DNA sequence analysis
homologue of the Bel-2 oncoprotein.";
Biochim. Biophys. Acta 1132:109-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=B-cell lymphoma;
MEDLINE=92379084; PubMed=1511008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92375724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis
                                                                                                            BL; D11382; BAA01978.1; J
BL; D11381; BAA01978.1; J
T11961; CAA78018.1; J
R; A37332; A37332.
R; S24390; S24390.
SP; Q07817; IMAZ.
                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waified and this statement is not removed. Usage by and for commercia itles requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   kidney, heart, ovary and brain, with the highest level thymus. In the embryo, highly levels expressed in all high levels in the bursa of Fabricius.

DOWAIN: The BH4 domain is required for anti-apoptotic for interaction with RAF-1 (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

SIMILARITY: Contains 1 Bcl-2 homology 3 (BH2) domain.

SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TaxID=9031;
                                 PF00452;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
BH4; 1.
7; BCL; 1.
                               Bc1-2;
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43,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bc1-2.
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                                                                                                                                                             JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissues with
                                                                                                                                                                                                                                                                                                                     a collaboration
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                    BCL2 BOVIN STANDARD
002718;
16-0CT-2001 (Rel. 40, C
16-0CT-2001 (Rel. 40, L
15-MAR-2004 (Rel. 43, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00265; BH4; 1.
TIGRPAMS; TIGR00865; BCL2-2;
PROSITE; PS50062; BCL2-FAM;
PROSITE; PS01080; BH1; 1.
PROSITE; PS011288; BH2; 1.
PROSITE; PS01258; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
                                                                                                                                                                                                                                                               Apoptosis BCL2.
                                                                                                                                                                                                                                                                                                                                                BOVIN
             -
                                                                                                        "Increased ratio of bcl-2/bax expression is associated with leukemia virus-induced leukemogenesis in cattle."; Virology 242:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis;
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                         Reyes R.A., Cockerell
                                                                                                                                                     MEDLINE=98162580; PubMed=9501056;
                                                                                                                                                               STRAIN=Holstein;
                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE
                                                                                                                                                                              EQUENCE
the apoptosis-activating factor (APAF-1) (By similarity). SUBUNIT: Forms homodimers, and heterodimers with BAX, BAI Bcl-X(L). Heterodimerization with BAX requires intact BH1
                               FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding release of cytochrome c from the mitochondria and/or by binding
                                                                                                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                                                                                               130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                   FROM N.A.
"Alstein; TISSUE=Thymus;
"Alstein; Tissue=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                  Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                     AEFTALYGDGALEEARRIREGNWASVRTVLTGAVALGALVTVGAFFASK
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                                                                                                                                                                                                                                                                          regulator
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TIGR00865; bcl-2;
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233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
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BH4_2; 1.
                                                                                                                                                                                                                  Bos.
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13, Last
Bcl-2.
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139
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                                                                                                                                                                                                                                                                                                               Created)
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_FAMILY;
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                                                                                                                                                                                                                                                                                     annotation update)
                                                                                                                                                                                                                                                                                                 sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 423.5;
Pred. No. 4.
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B -> S (IN REF. 2

GSAAASEVPPAEGLRP
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-> V (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233;
                                                                                                                                                                                                                           Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                                                                                                                                               233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                               bovine
BAK and
and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Matches 86
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01258; BH2; 1
PROSITE; PS01259; BH3; 1
PROSITE; PS01260; BH4_1;
PROSITE; PS50063; BH4_2;
                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                            Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2 FAMILY; 1. PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002475;
InterPro; IPR004725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                               NIAMOC
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cycochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for interaction with RAF-1 (By similarity).

PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
anti-apoptotic activity. Growth factor-stimulated phosphorylation
on Ser-70 by PKC is required for the anti-apoptosis activity and
occurs during the G2/M phase of the cell cycle (By similarity). Ir
the absence of growth factors, Bcl2 appears to be phosphorylated
by other protein kinases such as ERKs and stress-activated
kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: Proteolytically cleaved by caspases cleaved protein, lacking the BH4 domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains, and is necessary for anti-apoptotic activity. Al interacts with APAF-1, RAF-1 and TP53BP2 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intra membrane of the nuclear envelope and the endoplasmic reti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: The BH4 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U92434; AAB53319.1; -.
                              3
                                                           10
 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00337; BCL;
SM00265; BH4;
                                                                                       φ
                                                                                                                       86;
                                                                                                                                       Similarity
                                                                                           DTRALVADFVGYKLRQKGYVCGAG------
AAAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFR
                                                         DNREIVMKYIHYKLSQRGYEWDAGDAGAAPPGAAPAPGILSSQPGRTPAPSRTSPPPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR00865;
                         GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQ
                                                                                                                       Conservative
                                                                                                                                                                                   AA;
                                                                                                                                                                              30
68
72
97
145
192
223
223
250
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC12_BH.
BC12_BH4.
BCL2_family.
BC12_reg.
                                                                                                                                      41.4%;
38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    bc1-2;
                                                                                                                                                                                                                                                                                                                                         ane; Mitochondrion; Phosphorylation.
                                                                                                                                                                                    X
X
                                                                                                                      35;
                                                                                                                                                                              POLY-ALA.
BH3.
BH1.
BH2.
POTENTIAL.
POTENTIAL.
CASPASES) (BY S
PHOSPHORYLATION (BY PKC) (BY
ADIDDOAF98FFF11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is required for anti-apoptotic activity and
                                                                                                                      Score 416.5; DB
Pred. No. 2e-30;
5; Mismatches
                                                                                                                                                                                                                                                                                                            POLY-PRO
                                                                                                                                                 DB 1;
                                                                                                                       59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         during apoptosis. The
                                                                                                                      Indels
                                                                                                                                                 Length
                                                                                                                                                                                               BY SIMILARITY)
(BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intracellular reticulum (By
                                                                                                                                                    229;
                                                                                                                                                                                            SIMILARITY)
                                                                                                                      45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration -
                                                                                                                      Gaps
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RESULT 11
BCL2_RAT
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        the apoptosis-activating factor (APAF-1).

-Is SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BC1-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RAF-1 and TP53BP2 (By similarity).

-IS SUBCELIULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-IT TISSUB SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.

-ID OMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

-IP TM: Phosphorylation/dephosphorylation on Ser-70 regulates Bc12 anti-apoptotic activity and services activity. BCC is remired for the arti-apoptotic activity and anti-apoptotic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUB-Ovary;
MEDLINE=95129487; PubMed=7828536;
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
"Expression of members of the bcl-2 gene family in the immature recovery: equine chorionic gonadotropin-mediated inhibition of granucell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P49950, Q62837; Q64032;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castren E., Ohga Y., Berzaghi M.P., Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94193015; PubMed=8144041;
Sato T., Irie S., Krajewski S., Reed J.C.;
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95059917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adult rat brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "bcl-2 messenger RNA is localized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the caspases. Inhibits caspase activity either by preventing the
anti-apoptotic activity. Growth on Ser-70 by PKC is required for
                                                                                                                                                                                                                                                                                                                                                                                   caspases. Inhibits caspase activity either by release of cytochrome c from the mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-172 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=7969891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tzimagiorgis G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurons
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or-stimulated phosphorylation anti-apoptosis activity and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the immature rat
                                                                                                                                                                                                                                                                                                                                                                                      preventing and/or by k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                      binding to
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Best Local (
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PROSITE; PS01080; BH1; 1
PROSITE; PS01258; BH2; 1
PROSITE; PS01259; BH3; 1
PROSITE; PS01260; BH4 1;
PROSITE; PS50063; BH4 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00452; Bc1-2; 1.

Pfam; PF02180; BH4; 1.

SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGRFAMS; TIGR00865; bc1-2; 1
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CONFLICT
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EMBL; U34964; AAA77687.1; -.

EMBL; U34964; NOT ANNOTATE

EMBL; S74122; -; NOT ANNOTATE

PIR; 153744; 153744.

PIR; 167432; 167432.
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                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000712; Bcl2 BH.
InterPro; IPR003093; Bcl2 BH4.
InterPro; IPR002475; BCL2 family.
InterPro; IPR002475; BCL2 reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
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                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            titles requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: Proteolytically cleaved by Caspases during apoptosis. Cleaved protein, lacking the BH4 domain, has pro-apoptosic activity, causes the release of cytochrome c into the cytos promoting further caspase activity (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

SIMILARITY: Contains 1 Bcl-2 homology 4 (BH3) domain.

SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation Buropean Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no weekly non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. bephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
    130
                            82
                                                        70
                                                                                    28
                                                                                                               10
                                                                                                                                                                      84;
                                                                                                                                                                                  Similarity
VVEELFROGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and this statement is not removed. Usage by and the statement is not removed. Usage by and the community of the statement (See http://www.isb-sib.ch/announce/
                          VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                       SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSOLHLTPFTARGRFAT
                                                                                                            DNREIVMKYIHYKLSORGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART
                                                                                                                                         DTRALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                             236 AA;
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                            10
90
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                                                                                                                                                                                                                                                                                                                                                                                                 ransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -; NOT_ANNOTATED_CDS
                                                                            -VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                                              BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                       30
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230
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70
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164
                                                                                                                                                                                                                             26622
                                                                                                                                                                                41.1%;
36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _FAMILY;
                                                                                                                                                                                                                             ME.
                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion; Phosphorylation
                                                                                                                                                                                                                                    BH4.
BH3.
BH1.
BH2.
POTENVIAL.
POTENVIAL.
POTENVIATION (BY PKC)
PHOSPHORYLATION (BY PKC)
A -> R (IN REF. 2).
S -> Y (IN REF. 2).
S -> Q (IN REF. 2).
                                                                                                                                                                   Score 414; DB 1;
Pred. No. 3.4e-30;
4; Mismatches 62
                                                                                                                                                                                                                            -> Q (IN REF. 2)
E7688CB9071A872A
                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
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L outstation -
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RESULT 12
BCL2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P10417; P10418;
01-MAR-1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphatase 2A*.";
J. Biol. Chem. 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99059407; PubMed=9852076; Deng X., Ito T., Carr B., Mumby M., "Reversible phosphorylation of Bcl2 bryostatin 1 is mediated by direct i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92375724; PubMed=1508712; Eguchi Y., Ewert D.L., Tsujimoto Y. "Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in a variety of tissues including lymphoid adult and embryo."; nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the gene homologous to the human gene involved in follicular lympho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Negrini M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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BCL2 OR BCL-2.
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                                             IsoId=P10417-2; Sequence=VSP 000513; TISSUE SPECIFICITY: Expressed In a var DOMAIN: The BH4 domain is required for interaction with RAF-1.
                                                                                                                                                                                         MUNICIPAL NAME - NAME -
                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: membrane of the nuclea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49:455-463 (1987).
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                                                                                                                                                         IsoId=P10417-1;
    Phosphorylation/dephosphorylation apoptotic activity. Growth factor
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PubMed=9852076;
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                                                                                                                                                                                                     splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                  variety of tissues. for anti-apoptotic
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neuronal organs in
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                      regulates
regulates Bcl2
phosphorylation
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                                                                    activity and
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Best Local S
Matches 87
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GO; GO:0005829; C:cytosol; IDA.
GO; GO:00058189; F:apoptosis inhibitor ac
GO; GO:0005155; F:protein binding; IPI.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR002475; Bcl2 family.
InterPro; IPR00475; Bcl2 family.
InterPro; IPR00475; Bcl2 reg.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                          TICRFAMS; TICR00865; bcl-2; 1.

PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01250; BH4_1; 1.

PROSITE; PS01260; BH4_1; 1.

PROSITE; PS50063; BH4_2; 1.
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VARSPLIC
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SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                 DOMAIN
DOMAIN
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EMBL; M16506; AAA37282.1;
EMBL; M16506; AAA37281.1;
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                          Apoptosis; A
Phosphorylat:
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HSSP; Q07817; 1MAZ.
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87; Conser
                                                           DTRALVADFVGYKLROKGYVCGAG------PG-----
SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
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BH3.
BH1.
BH2.
POTENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC).
DAFVELYGESMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                34;
                                                                                          Score 413; DB 1;
Pred. No. 4.2e-30;
                                                                                                                                             GHK -> VGACLVE (in isoform
                                                                                                                                    /FTId=VSP
                                                                                                                        TIC=VSP_000513;
AA85EF6B0766BE0A_CRC64;
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                          activity;
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                                                                                59;
                                                                                                                                                                                                                                                    Mitochondrion;
                                                                                                    Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87002488; PubMed-2875799; Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for k 2/immunoglobulin transcript resulting from the translocation.";
MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stappleton M.J., Uddin T.B., Toshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McXernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM ALPHA).

MEDLINE=88196071; PubMed=2834197;
Seto M., Jaeger U., Hockett R.D., Graninger
Goldman P., Korsmeyer S.J.;

"Alternative promoters and exons, somatic mu
of the Bcl-2-Ig fusion gene in lymphoma.";
EMBO J. 7:123-131(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR 1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARI. Rieder M.J., Livingston R.J., Daniels M.R., Rieder M.J., Livingston R.J., Daniels M.R., Poe Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poe Schackwitz W.S., Sherwood J.K., Witrak L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL2_HUMAN STANDARD;
P10415; P10416; Q13842;
                                                                                                                                                SEQUENCE FROM
TISSUE=Testis;
                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                 translocation.";
Cell 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=87002488; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS ALPHA MEDLINE=86259760; PubMed=3523487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adult and embryo.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92375724;
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                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Res.
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characterization of the chic
f tissues including lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20:4187-4192(1992)
                                                                                                                                                              (ISOFORM ALPHA).
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uman follicular lyn
83:5214-5218(1986)
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.R., Montoya M.A., Chur, Poel C.L., Robertson
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lymphoma.
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neuronal org
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Naumovski L., Cleary M.L.;
"The p53-binding protein 53BP2 also interacts
"The p59-binding protein 53BP2 also interacts
cell cycle progression at G2/M.";
Mol. Ceil. Biol. 16:3884-3892(1996).
                                                                                                                                                                                                                                                                                                                   protein kinase pathway normally activated at G(2)/M.";
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Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=2036804; PubMed=10567572;
MEDLINE=2036804; PubMed=10567572;
Yamamoto K., Ichijo H., Korsmeyer S.J.;
"BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal "BCL-2 is phosphorylated and inactivated at G(2)/M.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ueno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON-HODGKIN'S LYMPHOWA SER-59 AND ILE-93.
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"Frequent incidence of somatic mutations in toncogenes of non-Hodgkin's lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length buman and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21260650; PubMed=11368354; Ruvolo P.P.; Deng X., May W.S.; "Phosphorylation of Bcl2 and regulation the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96251339; PubMed=8668206;
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Nature 369:321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conversion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91066924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVIEW ON PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH TP53BP2.
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the apoptosis-activating factor (APAF-1).
SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD,
Bol-X(I). Heterodimerisation with BAX requires intact BH1 a
domains, and is necessary for anti-apoptotic activity (By
similarity). Also interacts with APAF-1, RAF-1 and TP53BP2.
SUBCELLULAR LOCATION: Outer mitochondrial membrane, intrace
membrane of the nuclear envelope and the endoplasmic reticu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K., Hardwick J.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sion of Bcl-2 to a Bax-like death effector by caspases."; 278:1966-1988(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASPASES, AND MUTAGENESIS
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rsch D.G., Clem R.J., Ravi R.,
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nez G., Milliman C.,
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                                                                                                                                                                                    BAK and
and BH2
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Best Local S
Matches 87
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EMBL; M13995; AAA51814.1; ALT_SE
EMBL; M14745; AAA35591.1; --
EMBL; X06487; CAA29778.1; --
EMBL; X020759; AA026045.1; --
EMBL; BC027288; AAD2758 1; --
EMBL; S72602; AAD14111.1; ALT_SE
                                                                                                                                                                                                                                                                                                                                   PIR; B29409; TVHUB1.
PIR; C37332; TVHUA1.
PDB; 1G5M; 21-MAR-01.
PDB; 1GJH; 13-UN-01.
Genew; HGNC:990; BCL2.
                                                                                                                             InterPro; IPR000712; Bcl2 BH.
InterPro; IPR003093; Bcl2 BH4.
InterPro; IPR002475; BCL2 family.
InterPro; IPR004725; Bcl2 reg.
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                                                                                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity). PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

PISEASE: Involved in follicular lymphoma (FL) (also known as type to the cytosol structure) and considered to the cytosol structure caspase activity.

PISEASE: Involved in follicular lymphoma (FL) (also known as type to the cytosol structure) which involves BCL2 and immunoglobulin gene regions. BCL2 mutations found in non-Hodgin's lymphomas carrying the chromosomal translocation could be attributed to the Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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                                                                                                                                                                                      GO:0006959; P:humoral immune response; GO:0008285; P:negative regulation of c GO:0000074; P:regulation of cell cycle erPro; IPR000712; Bcl2_BH.
                                                                                                                                                                                                                                          GO:0005743; C:mitochondrial inner membrane; GO:0006189; F:appoptosis inhibitor activity; GO:0006916; P:anti-apoptosis; TAS.
GO:0006959; P:humoral immune response; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transitions.

SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1)
SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2)
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3)
SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4)
SIMILARITY: Belongs to the Bcl-2 family.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol.
                                                                                                                                                                                                                                                                                                                    151430; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WWW="http://www.infobiogen.fr/services/chromcancer/Genes/BCL2ID49.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              somatic hypermutation mechanism resulting in nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The BH4 domain is for interaction with RAF-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
Event=Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: Phosphorylation/dephosphorylation on Ser-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P10415-2; Sequence=VSP_000512; ISSUE SPECIFICITY: Expressed in a variety of tissues.
MAIN: The BH4 domain is required for anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P10415-1; Sequence=Displayed;
                      9
                                                          87;
                                                                            Similarity
DTRALVADFVGYKLRQKGYVCGAG----
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA51813.1; ALT SEQ.
AAA51814.1; ALT_SEQ.
AAA35591.1; -.
CAA29778.1; -.
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                                                          34;
                                                                        Score 412.5;
Pred. No. 4.
                                                         Mismatches
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                                                                                                                                                                                se; TAS.
f cell proliferation; 7
/cle; TAS.
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RESULT 14
BCL2_CRILO
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QJJV8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seguence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                         the appoptosis-activating factor (APAP-1) (By similarity).

-!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAA, BAK and Bc1-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Also interacts with APAP-1, RAF-1 and TP53BP2 (By similarity).

-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-!- DOWAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAP-1 (By similarity).

-!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bc12 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bc12 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A) of the similarity in the cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL2
            - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., MEDLINE=21092839; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.";
Biochem. Biophys. Res. Commun. 275:899-903(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20431763; PubMed=10973819;
Tomicic M.T., Christmann M., Kaina B.;
"Cloning and functional analysis of cDNA encoding the hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomicic M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cricetulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10030;
PM: Protectly ically cleaved by caspases du cleaved protein, lacking the BH4 domain, ha activity, causes the release of cytochrome promoting further caspase activity.

SIMILARITY: Contains 1 Bc1-2 homology 1 (BH SIMILARITY: Contains 1 Bc1-2 homology 2 (BH SIMILARITY: CONTAINS 1 BC1-2 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chem. Biophys. Res. Commun. 281:404-408(2001).
FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoletic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding trelease of cytochrome c from the mitochondria and/or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caspase-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRILO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1092839; PubMed=11181062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       longicaudatus (Long-tailed hamster) (Chinese hamster).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is cleaved in vitro and in cells by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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      (BH1)
(BH2)
                                                                                            during apoptosis.
has pro-apoptotic
me c into the cytor
      domain.
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XENLA AR11 XEI Q91828;

XENLA

STANDARD;

204

A

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
101-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Apoptosis regulator R11 (XR11).
Apoptosis regulator R11 (XR11).
Enclose regulato

Xenopodinae;

Xenopus

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RESULT
AR11_XE
AC QS
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Best Local
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TIGRPAMS; TIGR00865; bcl
PROSITE; PS50062; BCL2_F;
PROSITE; PS01080; BH1; 1
PROSITE; PS01258; BH2; 1
PROSITE; PS01259; BH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY:
-!- SIMILARITY:
-!- SIMILARITY:
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SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00337;
SMART; SM00265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004725; I
Pfam; PF00452; Bcl-2;
Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01260; BH4_1; PROSITE; PS50063; BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ271720;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro; IPR000712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC7383; JC7383.
; Q07817; 1MAZ.
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                      VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                                                                                                                                                  GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                    SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                         ----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                                                                       DTRALVADFVGYKLRQKGY------
                                                                                                                                                           GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK
                                                                                                                                                                                                         VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS PLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003093;
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90
133
184
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64
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236 AA;
                                                                                                                                                                                                                                                                                                                                             Conservative
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104
152
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26491
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Bcl2_Family.
BCL2_reg.
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_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                          MW ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion;
                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                       BH4.
BH3.
BH1.
BH2.
CLEAVAGE (BY CASPASE PHOSPHORYLATION (BY PHOSPHORYLATION)
                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.4e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 403;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                        (BY CASPASE-3 AND CASPASE-9).
YLATION (BY PKC) (BY SIMILARITY).
1EF3337228 CRC64;
                                                                                                                                                                                                                                                                                                                                                        .4e-29;
                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BH3)
(BH4)
                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                             Indels
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Search completed: March 25, 2004, 15:43:01 Job time: 11 secs
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Best Local Similarity
Matches 82; Conserva
                                                                                                                                                                                                                                                                                                                                  SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGRFAMS; TIGR00865; bCl-2; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01080; BH2; 1.

PROSITE; PS0062; BCL2 FAMILY; 1.

APOPLOS18; Transmembrane.

DOMAIN 101 120 BH1.

DOMAIN 152 167

TRANSMEM 181 198 POTENT
                                                                                                                                                                                                                                                                                                                       TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000712; Bc12_BH.
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR0032475; Bc12_family.
InterPro; IPR004725; Bc12_reg.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X82461; CAA57844.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                    184 RLLTI-VMLTGVFAL 197
                                                                                                    124 VESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFG
                                                                                                                             108 AESVNKEMEPLVGQVQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G
                                                                            166 NWASVRTVLTGAVAL 180
                                                                                                                                                        64 EATESFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC
                                                                                                                                                                                      48
                                                                                                                                                                                                                                      10 TRALVADFVGYKLRQKGYVC-------GAGPGEGPAADPIHQAMR 47
                                                                                                                                                                                                                ഗ
                                                                                                                                                                                 AAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFEVEGAALC 107
                                                                                                                                                                                                           SRDLVEKFVSKKLSO-NEACRKFSNNPNPMPYLMEPSTSERPGEGATOGIVEBEVLOALL 63
                                                                                                                                                                                                                                                                                                                       204 AA;
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                     23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                36.8%; Score 371; DB 1; Length 204; 42.1%; Pred. No. 2.2e-26; tive 25; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                    BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                               Gaps
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                                                                                                     183
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                      GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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Qy 141 SGGWAEFTALYGDGALEBARRIREGNWASVRTVLTGAVALGAL	CY 81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWWVAYLETRLADW	Qy 29 CGAGPGEGPAADPLHQAMRAAGDEFETRFRRTI	Qy 11 RALVADFVGYKLRQKGY	Query Match 42.6%; Score 428.5; DB 2 Best Local Similarity 41.3%; Pred. No. 2.9e-32; Matches 93; Conservative 22; Mismatches 57	YY NA KAM's EMBL:X83574; NID:g695622; PIDN: apoptosis regulator, inhibitory	J:Ul0101; NID:g506647; G.Y.; Takatsu, K.; Ok ata Library, November 1 bits anti-IgM-induced	A;ACCESSION: 14905 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA	153, 4388-4398, 1994 ning and molecular characterization of number: 149055, MUID:95052604, PMID:79	(house mouse)   Juence revision 02-Jul-1996   2866	л∟+	30 143 14.2 177 2 S54778 31 141 14.0 255 2 JC7567 32 137.5 13.7 143 2 I38921 33 118 11.7 175 2 I39055 34 112 11.1 350 2 A47476 35 10.5 10.4 175 2 I39055 36 91.5 9.1 301 2 T36534 37 89 8.8 185 2 B83217 38 87 8.6 3433 1 GNWVKV 39 85 8.4 279 2 AI2598 40 84 8.4 279 2 B97381 41 84.5 8.4 279 2 B97381 42 83.5 8.2 1440 1 GNWVJF 44 82.5 8.2 3432 1 GNWVJF 45 81.5 8.1 354 2 S52040	
AVALGAL 183     :       229	SVNKEMEPLYGQVQEMYVAYLETRLADWIHS 140	PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80 	ERETPSAINGNPSWHLADSPAV 65	; Length 233; ; Indels 53; Gaps 4;	CAA58557.1; PID:g695623 type	PIDN:AAAB2173.1; PID:g506648 uma, M. 994 apoptosis in an immature B cell line thro	4	mouse bcl-x in B and T lymphocytes. $33517$	#text_change 28-Jul-2003		NR-13 protein - qu Mc1-1a protein - z bc1-2-associated p Bc1-2 related - hu BCL2 homolog MCL1 hemopoletic-specif probable lipase/es hypothetical prote genome polyprotein dihydrodipicolinat dihydrodipicolinat glutamate-ammonia DNA binding protein genome polyprotein genome polyprotein genome polyprotein Gin 1.1 protein -	

RESULT 2 84/537 apoptosis regulator bcl-xL - human AP,Alternate names: bcl-2-related protein N;Contains: apoptosis regulator bcl-xS

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BCL-X protein - 1
C;Species: Rattus
C;Date: 07-May-19
C;Accession: S517
                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-233 <MIC>
A; Cross-references: EMBL: X82537; NID: g607176; PIDN: CAA57886.1;
A; Experimental source: embryonic; brain
A; Accession: S51762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted
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A;Title: bcl-x, a bcl-2-related gene that A;Reference number: A47537; MUID:93364977;
                                           O.A
                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
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A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176;
A;Experimental source: embryonic; brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-69,'G',71-125,189-233 <BO2>
                                                                                   A;Note: smaller form due C;Genetics:
                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S51761
A;Accession: S51761
                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Michaelidis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Homo sapiens (man)
;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
;Accession: B47537; C47537
;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Rattus norvegicus (Norway rapate: 07-May-1995 #sequence_revision)
Accession: S51761; S51762
                                           Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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    Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGATAHSSSLDAREVI PMAAVKQALREÄGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
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                                             159
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                                         apoptosis regulator,
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                                                                                                        to splicing
  42.2%;
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  Score
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Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                         November 1994
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                                       inhibitory type
  424.5;
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                                                                                                                                                  PIDN: CAA57887.1;
  B
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2
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  233;
                                                                                                                                                PID:g607178
                                                                                                                                                                                                                                                                          PID: g607177
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R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, Blochim. Blophys. Acta 1132, 109-111, 1992
A;Title: Molecular cloning and DNA sequence analysis A;Reference number: S24390; MUID:92379084; PMID:15110
A;Accession: S24390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993
C;Accession: A37332; S35453
R;Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acide Res. 20, 4187-4192, 1992
A;Title: Tsolation and characterization of the chic A;Reference number: A37332; MUID:92375724; PMID:150
A;Accession: A37332
                                                                                                        transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A; Residues: 1-233 < EGU>
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                                                                                             ;Accession: S24390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                        AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                      DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA
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                                                                                                                                                                                                                                                                                                               ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
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38.0%; Pre
vative 32;
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Pred. No. 8.3e-32;
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PMID:1511008
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PMID:1508712
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-58, 'T', 60-116, 'R', 118-239 < CLE>
A; Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID
R; Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wri
Oncogene Res. 2, 263-275, 1988
A; Title: Consequences of the t(14;18) chromosomal translocation
A; Reference number: A27622; MUID:88217344; PMID:3285301
A; Accession: A27622
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Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, a A;Reference number: A29409; MUID:86259760; PMID:3:
                                                                                                                                                                                                                  A;Title: Cloning and structural analysis of cDNAs for bA;Reference number: A24428; MUID:87002488; PMID:2875799 A;Accession: A24428
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A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A;Cross-references: GB:NI3994; NID:9179366; PIDN:AAA51813:1; PI
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett,
EMBO J. 7, 123-131, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transforming protein bcl-2, splice form alpha - human c;Species: Homo sapiens (man)
C;Date: 31-Dec:1988 #sequence revision 07-Jun-1996 #text change C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
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                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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A; Residues: 1-239 < EGU>
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A;Title: Isolation and characterization of
A;Reference number: A37332; MUID:92375724;
A;Accession: C37332
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A;Residues: 1-232 <CAZ>
A;Cross references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: mitochondrion; transmembrane protein
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                                                                                                                                                                                                                                                                                     Cleary, M.L.; Smith, 19-28, 1986
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sidues: 1-58,'T',60-239
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37.7%; Pred. No. 6.3e
tive 32; Mismatches
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PMID:1508712
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Wright, J.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Goldman,
                                                                                     in follicular lymphoma:
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                                                                                                                                                                                                                                                             hybrid
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                                                                                                                              J.J.;
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                                                                                                                                                                                                                                                             bcl-2/immunogi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bc1-2,
                                                                                                                            Bakhshi,
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C;Accession: 167432
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bc1-2 gene family in onstitutive bc1-2 and bc1-xlong messenger ribonucleic acid A;Reference number: 153295; MUID:95129487; PMID:7828536
A;Accession: 167432
                                                                                                                                                                                                                                                                                                                                                               A; Cross-1017:
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from A;Molecule type: mRNA A;Residues: 1-236 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
167432
                                                                      밁
                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL-2 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl apoptosis regulator, inhibitory type C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    片
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A;Map position: 18q21.3-18q21.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function:
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                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; Superfamily: bcl apoptosis regulator, inhibitory type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                   Similarity
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                                    GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                          VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                DTRALVADFVGYKLRQKGY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNREIVMKYIHYKLSORGYEWDAGDVGAAPPGAAPAPGIFSSOPGHTPHPAASRDPVART
                                                                        VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                 ----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR
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37.0%;
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-PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                 Score 412; DB 2;
Pred. No. 9.8e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 412.5; DB Pred. No. 9e-31;
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                                                                                                                                                                                                                                                                                                                                Length 236;
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gene bc1-z p-

G:Species: Rattus norvey-

C:Species: Nay-1998 #sequence_revie.

C:Date: 29 May-1998 #sequence_revie.

C:Accession: 153744

R:Sato, T.; Irie, S.; Krajewski, S.

Came 140, 291-292, 1994

Came 140, 291-292, 1994
                                                                                                                                                                                                                                    A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expre A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
TVMSA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transforming protein bcl-2-alpha - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003 C;Accession: A25960; E37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the A;Reference number; I53744; MUID:94193015; PMID:8144041
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C;Superfamily:
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                                                                                                                                                                                A;Residues: 1-33,
                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                    Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and A;Reference number: A90893; MUID:87187643; PMID:30324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Negrini, M.;
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                                                                                                                                          A;Gene: BCL2
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      Best Loc
Matches
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Best Local S
Matches 83
                                                                                                                                                                                              Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                        ;Molecule type: DNA
;Residues: 1-236 <NEG>
                                                                          Superfamily: bcl apoptosis regulator, inhibitory type; Keywords: alternative splicing; mitochondrion; transf.
                    Query Match
Best Local
                                                                                                                    Introns: 192/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        i, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.;
455-463, 1987
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                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĠĠ₩DAFVEĹŶĠ----PSMŔPĹFDFSŴĹŚĹKTĹĹSĹÁL-VĠÁCIŤĹĠÁYĹGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTRALVADFVGYKLROKGY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                                                          ,'E',34-220,'AL',223-236 <EGU>
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision 29-May-1998 #text_change 28-Jul-2003
40.3%; Score 406; DB 1; Length 236; 37.1%; Pred. No. 3.5e-30; tive 33; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.4%;
35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 407; DB 2;
Pred. No. 2.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitory type
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                                                                                                                                                                                                                  shown;
                                                                            transforming protein;
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                                                                                                                                                                                                                                                                          expression
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                                                                              transmembrane
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R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Tile: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487; PMID:7828536
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-233 < RES >
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: I67431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Rattus norvegicus (Norway rat);
;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                  Matches
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185
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                                141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
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                                                                                                         81
                                                                                                                                            66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE
                                                                                                                                                                                 29 CGAGEGEGEAAD-----PLHQAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFT
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                                                                                                                                                                                                                                                            11 RALVADFVGYKLROKGY-----
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                                                                                                  QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                       RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWREIVMKYIHYKLSORGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART
                                                                     QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWWVAXLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPIRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
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                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                 40.2%;
                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                 Score 404.5; DB 2;
Pred. No. 4.8e-30;
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                                183
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RESULT JC7383

B-cell lymphoma 2 protein - Chinese hamster C;Species: Cricetulus griseus (Chinese hamst C;Date: 17-Nov-2000 #sequence\_revision 17-NC C;Accession: JC7383 hamster) 17-Nov-2000 #text\_change 28-Jul-2003

R;Tomicic, M.T.; Christmann, M.; Kaina, B. Biochem. Biophys. Res. Commun. 275, 899-903, A;Title: Cloning and functional analysis of a A;Reference number: JC7383

cDNA encoding 2000

the

hamster

Bcl-2 protein

A; Accession: JC7383 A; Contents: Ovary

P

A; Molecule type: mRNA A; Residues: 1-236 <TOM> A; Cross-references: GB: AJ271720 C; Comment: This protein has ant C; Genetics: has anti-apoptotic function, and supports cell survival

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bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-701-1996 #sequence_revision
C;Accession: 149057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C;Accession: A47537
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C;Superfamily: bcl
C;Keywords: B-cell
                                              R; Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A47537;
A;Accession: A47537
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A; Title: bcl-x,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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                                                                                                                                   I49057
                                                                                                                                                   RESULT
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. Immunol. 153, 4388-4398, 1994
;Title: Cloning and molecular characterization of mouse
;Reference number: I49055; MUID:95052604; PMID:7963517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:Z23110;
Superfamily: bcl apoptosis re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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bcl-x, a bcl-2-related gene that f
bcl-x, A47537; MUID:93364977;
                                                                                                                                                                                                 186
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                                                                                                                                                                                                                                                               LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDFWIQENGGWV
                                                                                                                                                                                                                                                                                                                             VHRSSLEVHEI VRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
                                                                                                                                                                                                                                                                                                                                                                                                                            RALVADFVGYKLRQKGY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                                               LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                             -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
                                                                                                                                                                                                                                                                                                                                                                                              RELVIDFVSYKLSORGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT
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nilarity 35.3%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 378; DB 2; Length 190; 43.8%; Pred. No. 1.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
egulator, inhibitory type
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Pred. No. 6.7e-30;
14; Mismatches 64;
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                                                                                   02-Jul-1996
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                                                                                   #text
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               T lymphocytes.
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   RESULT
B37332
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apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl
                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-227 <BAN>
A;Cross-references: GB:U72398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschac Biochem. Biophys. Res. Commun. 248, 147-152, 1998 A;Title: Identification of a human cDNA encoding a novel A;Reference number: JE0203; MUID:98340865; PMID:9675101
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
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                             SGGWAEFTALYGDGALEEARR 161
                                                             QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184
                                                                                         QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEFLVGQVQEWMVAYLETRLADWIHS 140
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Pred. No. 2.3
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A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl apoptosis regulator, inhibitory type
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C;Species: Gallus gallus (chicken)
C;Daec 03-Mar1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
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R;Bquchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Rv.Bquchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Rv.Bquchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Rv.Cleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: B37332
A;Status: nucleic acid sequence not shown
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Local Similarity 38.4%; Pred. No. 1.4e-25;
hes 71; Conservative 21; Mismatches 49; Indels 44; Gaps
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                                                                                                                                                                                                                       130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189
                                                                                                                                                                                                                                                                                                                                                                                42 ------LHQAMRAAGDEFETRERRTFSDLAAQLHVTPGSAQQRFTQVSD 84
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Aaw97392 The human
Aaw97397 The human
Aaw97397 Human Bcl
Aay05532 Human Bcl
Aay05531 Mouse Bcl
Aaw97391 The rat b
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Aaw59884
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Bcl-Xl-DT
Wild type
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Aau76553	Abg78478	Abg78479	Aab74127	Aab35130	Aaw87810	Aau76554	Aab35131	Aag79760	Aag64037	33	Aaw19396	Abr83557	Abr83558	Ade62491	Ade62493	Ade62921	-7	Aag64262	Aab73303
	Human B	Human Bc	Human bc	Human Bc		Murine	Murine Bc						TolA-BCL	. Rat Prot	Human Pro	. Rat Prot	Protein	Human Bc	Rat wild

## ALIGNMENTS

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RESULT 1
AAYOSS30
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AC AAYO
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N-PSDB; AAX25132.
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The present sequence is human Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Wethods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise

Claim 2; Page 33; 52pp; English.

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RESULT 2
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ID ADD44742
AC ADD4

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Matches 193;
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                     claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                      The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                               New composition comprising preparing a medicament for
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ANK; Q92843.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 193;
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Nucleic acids encoding B-cell lymphoma-y protein - unrecombinant protein for use in treating uncontrolled

useful

producing

growth

1998-446079/38. DB; AAV28334.

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                                                                                                                   23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; agging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW97392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 193
                                                                Guastella
                                                                                                                                                           25-NOV-1997;
                                                                                                                                                                                     16-MAR-1999.
                                                                                                                                                                                                               US5883229-A
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         The human bcl-y protein.
                                                                                           (COCE-)
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                                                                                           COCENSYS INC.
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                                                                                                                   96US-0012201P
97US-00798897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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Pred. No. 5e-102;
0; Mismatches 1;
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WPI; 1999-214150/18. N-PSDB; AAX15946.

Novel bcl-y homologues

of the

rat and human bcl-2 protein - useful

for

COTY S,

Adams

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Gibson LM,

Holmgreen

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(AMRA-)

AMRAD OPERATIONS PTY LTD

Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.

Human bcl-w protein

Homo sapiens

02-OCT-1997. WO9735971-A1

27-MAR-1996; 27-MAR-1997;

96AU-00008965 97WO-AU000199

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                               AAW36047 standard; protein; 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulating programmed cell death.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATPASAPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALVIVGAFFASK 193
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Pred. No. 5e-102;
0; Mismatches (
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RESULT 6
AAY05532
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     N-PSDB; AAX25134
                              WPI; 1999-243890/20
                                                                                Cory
                                                                                                                                                                                                                                                                                                    25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatogenesis; animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Bcl-w protein essential
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inhibit cell
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N-PSDB; AAT96577.
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                                                                                                                                                                                             16-SEP-1997;
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                                                                                Adams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry
                                                                                <u>_</u>
                                                                                                                                                                                             97AU-00009228
                                                                                                                                                                                                                                               98WO-AU000764.
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                                                                                                                                        MEDICAL RES WALTER & ELIZA.
                                                                                Print
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Pred. No. 8.3e-102;
1; Mismatches 1;
                                                                                Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for spermatogenesis.
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protein
                                                                                 An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.
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Disclosure; Page 37; 52pp; English

The present sequence is described of a derivative of human Bcl-w (see also AAY0533), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, can induce intertility enhancing or otherwise facilitating spermatogenesis inducing, ls, or which

Sequence 193 AA;

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91; Conservative
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                 GALVTVGAFFASK 193
                                                                     QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                   QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                            MATPASAPOTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
 GALVIVGAFFASK 193
                                                                                                       FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                           99.3%;
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                                                                                                                                                                                                             Score 1000; DB 2;
Pred. No. 8.3e-102;
1; Mismatches 1;
                                                                                                                                                                                                                                        Length 193;
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## RESULT 7 ARXO5531 ID AAXY XX AAYC XX AAYC XX Spel DE Mous XX Spel DE Mus XX Spel DE Mus XX IN WO99 25-M 27 16-5 27 16-5 27 16-5 27 YAX XX IN WO91 DE WFIL Spermatogenesis; Mouse Bcl-w protein 05-JUL-1999 AAY05531 AAY05531 standard; animal model. (first Bcl-3; protein; essential entry) Bcl-2; 193 for spermatogenesis. mouse; B fertility; infertility;

WPI; 1999-243890/20

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ELIZA Koentgen

16-SEP-1997;

97AU-00009228 98WO-AU000764.

HALL INST MEDICAL RES

16-SEP-1998;

25-MAR-1999 WO9913710-A1

N-PSDB; AAX25133.

animal model exhibiting reduced otein associated with Bcl-w.

levels

of a

Bcl-w protein

and/or

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RESULT 8
AAW97394
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Best Local Simi
Matches 191;
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                                                                                                                                                                             Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
 23-FEB-1996;
11-FEB-1997;
                                                  25-NOV-1997;
                                                                                    16-MAR-1999
                                                                                                                   US5883229-A
                                                                                                                                                                                                                                                                                                                       Mammalian bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97394 standard; protein; 192
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
96US-0012201P.
97US-00798897.
                                                 97US-00978523.
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Pred. No. 8.
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3.3e-102;
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RESULT 9
AAWG1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a mammalian bcy-1 protein. The grecification describes rat bcl-y protein (Rbcl-y) and human bcl-y components (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein (Lbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein chought to be involved in programmed cell death (appptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death components in the strokes, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular components, head trauma, Alzheimer's Disease, neural and muscular components, result induced cell death, aging, spinal cord injuries and confident as a result of triggers which may or may not be apparent. They can also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 191;
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Best Local
                                                                                                                                                                                                                                                                                                                  Rat bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-1998
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                                                                                                                                                                                                                                                      bcl-y; bcl-2;
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Matches 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding B-cell l recombinant protein for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-446079/38.
N-PSDB; AAV28333.
                                                                                                             Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   death is desired
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                                                                                                                                                                                                                              The rat bcl-y protein
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                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 3A; 27pp; English
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                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-cell lymphoma-y protein - useful r use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 996; DB 2; 1
Pred. No. 2.3e-101;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and cc Hbcl-y are homologues of the bcl-2 protein thought to be involved in corrections may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used to treat subjects suffering from: strokes, head trauma, correctably multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis correctably multiple sclerosis or premature cell death as a result of criggers which may or may not be apparent. They may also be used in this cord injuries and injuries for an extended cord in contrast, if they act as cell death as a result of period. In contrast, if they act as cell death stimulators, Rbcl-y and Ebcl-y may be used to treat conditions associated with prolonged cell conditions conditions associated with prolonged cell conditions conditions conditions conditions conditions conditions
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulating programmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel bcl-y homologues of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX15945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guastella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1996;
11-FEB-1997;
                                                                                            Sequence 193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present seguence represents rat bcl-y protein (Rbcl-y).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-214150/18
      Similarity
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97US-00798897.
   98.9%;
98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell death.
   Score 996; DB 2;
Pred. No. 2.3e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
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                                   Length 193;
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                      181
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181
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                                                                                                                                                           1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                         FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                               QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                              FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                       GALVIVGAFFASK 193
                                              QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEBARRLREGNWASVRTVLTGAVAL
                                                                                                                                             MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
 GALVIVGAFFASK 193
                                                                                                                                                                                              Conservative
                                                                                                                                                                                             1;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                               Indels
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                                                                                                                                                                                              Gaps
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RESULT 11
AAW97393
ID AAW97397
XX AAW97
XX AAW97
XX Prote
XX Progr
XW Rat E
XW Rat E
XW Multil
KW multil
Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; agging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
                                                                                                                                                                                                                                                                                         AAW97393
                                                                                                                                                Protein sequence of the specification.
                                                                                                                                                                                               20-MAY-1999
                                                                                                                                                                                                                                                                                         standard; protein;
                                                                                                                                                                                               (first entry)
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25-NOV-1997;

97US-00978523

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RESULT 12
AAY05533
ID AAY05
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AC AAY05
XX
DT 05-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein CC thought to be involved in programmed cell death (apoptosis and necrosis). CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated CC with a disruption of the cell death pathway. If they act as cell death CC inhibitors, they may be used in therapies to treat subjects suffering CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular CC degenerative diseases (especially multiple sclerosis) myocardial CC infarction, vitally induced cell death, aging, spinal cord injuries and CC amyotrophic lateral sclerosis- conditions where cells under go premature CC eall death as a result of triggers which may or may not be apparent. They CC may also be used in this way to develop cell lines which remain viable in CC culture for an extended period. In contrast, if they act as cell death CC with prolonged cell life span such as cancer (especially kaposi's sarcoma CC and lung cancer) and auto/hyperimmune diseases. They may also be used to couse cell death in, and hence control, parasites
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 192 AA;
                               AAY05533;
                                                                  AAY05533 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 19-20; 26pp; English
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11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1997;
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                                                                                                                                                    ALVIVGAFFASK 192
                                                                                                                                                                                ALVTVGAFFASK 193
                                                                                                                                                                                                                                                   VQBWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG
                                                                                                                                                                                                                                                                                      SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ
                                                                                                                                                                                                                                                                                                         SDLAAQLHVTPGSAQQRFTQVSDELFQGGFNWGRLVAFFVFGAALCAESVNKEMEPLVGQ
                                                                                                                                                                                                                     VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG
                                                                                                                                                                                                                                                                                                                                                       ATPASTPOTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRTE
                                                                                                                                                                                                                                                                                                                                                                                        ATPASAPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRTF
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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97US-00798897.
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                                                                  protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                         98.4%;
98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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Pred. No. 8.1e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 192;
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05-JUL-1999

(first entry)

RESULT 13
AAW36048
ID AAW36
XX
AC AAW36

AAW36048 standard; protein;

168

AAW36048

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                                                                                                                                                                                                                                                                                                                                                                         The present sequence is described of a derivative of mouse Bcl-w (see Cl also AAY05531), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The derivative lacks the 24 N-terminal amino acids of Bcl-w. The invention relates clearly to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one callele of the human or murine bol-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, capitals of a characteristics.
                                                                                                                                                                                                                                                                Matches 183;
                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 39; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-243890/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Bcl-w protein deritvative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1997;
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                                                                                                                                                                                                                                                                             ocal Similarity
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180
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                      GALVTVGAFFASK 193
                                                                                    QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                   FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                               MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                         MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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GALVIVGAFFASK 192
                                                              QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRIREGNWA-VSTVVTGAVAL
                                                                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                             95.2%;
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                                                                                                                                                                                                                                                                             Score 958.5; DB 2; Pred. No. 3.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibson L,
                                                                                                                                                                                                                                                                Mismatches
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RESULT 14
AAO18223
ID AAO18
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AC AAO18
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DT 18-SE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a novel protein, bcl-w, encoded by the mouse bcl -2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid
inhibit cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gs su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                      18-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cory s,
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                                                                                AA018223
                                                                                                          AAO18223 standard;
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                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                     161;
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                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                      61
 apoptotic signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT96578
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                                                                                                                                                                                                   QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                                                                                MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                         MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                        QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA
                                                                                                                                                                                                                                                      FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerative disease
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding apoptosis related gene survival, e.g. for treatment of
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50-51; 86pp; English
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                                                                                                         protein; 190
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                                                                                                                                                                                                                                                                                                                                               86.1%;
95.8%;
                            domain
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                            related protein
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Pred. No. 3.3e-87;
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  protein; Bcl-Rambo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bcl-w - used to induce cancer and degenerative
                                                                                                                                                                                                                                                                                                                                                             Length 168;
                                                                                                                                                                                                                                                                                                                                     Indels
    BHNo domain;
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RESULT 15 AAW59884 ID AAW59

AAW59884 standard; protein; 365

**XXXXXXXXX** 

Amino 20-NOV-1998

acid

(first

entry)

Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.

of the cDNA clone Bcl-like

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                                                                                                                                                                                                                                                                 Matches 170;
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of the human Bcl-Rambo apoptotic transcription factor, particularly the BHNo domain. The sequences are useful in the treatment of diseases caused by incorrectly regulated intracellular signal transduction, including cancers, neurodegenerative diseases (e.g. Alzheimer's or Parkinson's diseases), muscular dystrophy, viral infections (including human immunodeficiency virus), autoimmune disease, septic shock, graft versus host disease and acute hepatitis. The present sequence is a procein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; neurodegenerative disease; Alzheimer's disease; cytostatic; nootropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory; immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock; Parkinson's disease; muscular dystrophy; HIV; viral infection; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-2000; 2000DE-01061766.
04-JAN-2001; 2001DE-01000280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              graft versus host disease; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                 Sequence 190 AA;
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                                                                                                                                                                                                                                                                                   Local
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178
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                                                                                       QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                MATPASAPXTXAXVAD-XGYKLRQKGYVNGAGPGXGPAAD-XHQAXRAAGXEFETRFXRT
                                                                                                                                                                                                                                MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                GALVIVGAFFASK 193
                                                                                                                                FSDLAAQLHVTPGSAQQRFTQVSDELFQGXPNWGXXXAFFVFGAAXCAESVNXEMEPLVG
 GALVTVGAFFASK 190
                                                                QXQEXMVAYLETXLAX-IHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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Pred. No. 4.1e-82;
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Search completed: March 25, 2004, 15:42:28 Job time : 52 secs
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Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies or tumours.
                                                                                                                                                                                                                                                                                                                                               Sequence 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                can also be used for detection and diagnosis
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21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC. (AUCK-) AUCKLAND UNISERVICES LTD.
                                                                                                121 QVQEWMVAYLETRLADWIHSSGGW 144
                                                                      121
                                                                                                                                                             61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                              1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGBGPAADPLHQAMRAAGDBFETRFRRT 60
                                                                                                                                                                                                          1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFETRFRRT 60
                                                                    QVQEWMVAYLETRLADWIHSSGGW 144
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97US-0034205P.
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length: 2000000000
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AY421022 Mus muscu
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                                                                                       Description
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SOURCE
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            2 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal, Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 582)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Carqill,M.
                                                                                                                       gene trios
Science 302 (5652),
                                                                                                                                                                                                                                                                                                  Mus musculus
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   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
AY421022
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AY421020 Homo sapi
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BE793530 601590016
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AKC013244 MUS muscus
BI770566 603060362
BG298789 602396527
CB578463 AMCNNUC: M
AW258810 um74a02. y
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

IRL Nature 420, 563-573 (2002)

ICE 6 (Dases I to 1949)

A Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Hiramoto, K., Kasukawa, T., Hori, F., Imotani, K., Nojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Sakai, K., Shibata, X., Shibata, X., Shibata, X., Shibata, Y., Shinagawa, A., Shiraki, T., Sagaki, D., Shibata, X., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, T., Sogabe, Y., Sinestion Research Group, RIKEN (Benomic Sciences Center (GSC), RIKEN), Laboratory for Genome Exploration Research Group, RIKEN (Benomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kingawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Fax:81-45-803-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB29912.1"
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GAALCASSVNKEMEPLVGQVQDMYVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="testis"
/clone_Tib="RIKEN full-length
/dev_stage="adult"
132._.713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="FANTOM_DB:4930488D08"
/db_xref="MGI:1897773"
/db_xref="MGI:1897773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed
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/clone="4930488D08"
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Pred. No. 4.7e-132;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                      Mature 420, 53-573 (2002)

Be (bases 1 to 3487)

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakwa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Furuno,M., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Hiraoka,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ckazaki,Y., Okido,T., Owa,C., Saito,R., Saito,R., Sakai,C., Sakai,X., Sano,H., Sasaki,D., Shibata,Y., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Shibata,Y., Shibata,Y., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Ali Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama, Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashixo, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Ckazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK004680 3487 bp mRNA linear HTC 20 Mus musculus adult male lung cDNA, RIKEN full-length enric library, clone:1200009L24 product:Bcl2-like 2, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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                                                        RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yo
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Mammalia; Eutheria; Rodentia;
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Fax:81-45-503-9216
Please visit our w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN
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Encyclopedia Project of Genome Exploration Research Gro
Genomic Sciences Center and Genome Science Laboratory i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
                                                                                                                                      CAGGTTTCCGACGACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                           AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCCTGGGGAAGGCCCAGCCGCCGAC
CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                      GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
                                                                                                               CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                       TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                     CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                                                                                                               AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCCAGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
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/clone Tib="RIKEN full-length
/dev_stage="adult"
209. ..790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3487
/note="putative"
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/brotein_id="bab23468.1"
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/translation="matpastpotralvadfvgyklrqkgyvcgagpgegpaadplhq
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Amraagdfetriffrerffesdlaaqlhvtpgsaqqrftqysdelfqggalefyk
gaalcaesvnkemeplvgqvqdmmvayletrladwihssggwaeftalygdgalefar
RLREGNWASTRTVLTGAVALGALVTVGAFFASK"
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(MGD[MGI:108052)
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:1200009L24"
/db_xref="MGI:1896837"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="putative"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Fukuda,S., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojina,Y.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojina,Y.,
Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Kanagawa 230-0045, Japan

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                                                                                                                                                                                                                                                                   RCE 1 (Dases 1 to 969)

RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.P., Forrest, A., Frazer, K.S., Gassterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, L.J., Jarvis, B.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, J.V., Lee, Y., Lethard, B., Lyons, P.A., Maglott, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Ravasi, T., Reed, J.C., Reed, D.J., Pertea, G., Pesole, G.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ranachandran, S.,

Fallai, R., Wanhestedt, C., Wang, Y., Watanabe, Y.,

Wella, C., Wilming, L.G., Wynshaw-Boris, A., Yangdsawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayateu, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Shinagawa, A., Shiraki, Y.

Shinagawa, A., Shiraki, Y.

Shinaki, Y.

Shiraki, Y.
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BY715200 RIKEN full-length enriched, acu.
Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                      Nature 420, 563-573 (2002) 22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY715200.1 GI:27128317
                                                                                                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                  61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (200)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                CCGCTGCAAGCCATGCGGGCTGCTGGAGAGAGTTTGAGAGCCATTTTCCGCCGCCACC
                                                                                                                                                                                                                                                                                           AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
                                                                  CAGGTTTCCGACGAACTTTTCCAAGGGGGGCCCTAACTGGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                         TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="RIKEN full-length enriched, adult male testis /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue
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TITLE
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                                                                                                                                  567;
  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CNNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5', mRNA sequence.
BU503850
BU503850.1 GI:22810083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUS03850
967 bp mRNA linear EST 12-SEP-2002
AGENCOURT 10030867 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491566
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                                                                                                                                                         Similarity
  ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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                                                                                                                                    Conservative
                                                                                                                                                                                                                                       /clone="IMAGE:6491566"
/tissue_type="retina"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC 94"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 %b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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                                                                                                                                                         86.7%;
96.8%;
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                                                                                                                                                         Score 503.6; DB Pred. No. 1e-117;
                                                                                                                                    Mismatches
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This is the Clone from		source	
Ingolstaed	d on alignment.	FEATURES	
	Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them	COMMENT	
TITLE EST (Ansor	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	TITLE JOURNAL	
REFERENCE 1 (bases	<pre>Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.</pre>		
ORGANISM Homo sapie Eukaryota;	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	AUTHORS	
	1671302 2 (bases 1 to 582)	PUBMED	
VERSION AL157542.1	gene trios Science 302 (5652), 1960-1963 (2003)	JOURNAL	
DKFZ9761D0	Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous	TITLE	
AL157542 LOCUS AL157542 DEFINITION DEFENDA	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	AUTHORS	
RESULT 7	Mammalia; Eutheria; Primates; Catarrnini; Hominidae; Homo.  1 (Dases 1 to 582)  Claim C Classific Nielson B Thomas B Kejariwal A	REFERENCE	
Db 541 ĠĠĠĠĊĊĊT	Craniata; Vertebrata; I	ORGANISM	
Qy 541 GGGGCCCT		SOURCE	
Db 481 cerciece	AY421020.1 GI:39776977	ACCESSION VERSION	
Qy 481 CGTCTGCG	Homo sapiens BCLdL4 gene, Vikiuhi ikawackiri, pairtai acquence, genomic survey sequence.	DEFINITION	
Db 421 AGTGGGGG	5	AY421020 LOCUS	
Qy 421 AGTGGCGG		RESULT 6	
Db 361 CAAGTGCA	670 ACTGGGGGCCCTGGTAAGGGGCCTTTTTTGCTAGCAAGTG 715	Db 6	
Qy 361 CAAGTCCA		0у 5	
301	610 CGGCGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGC 669	Db 6	
301	478 CGGCGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGAC-GGGGGCCGTGGGC 536	Ογ 4	
Db 241 CAGGTCTC	50	Db 5	
Qy 241 ÇAGGTTTC		Qy 4	
Db 181 TTCTCTGA	490 CAAGTGCAAGATTGGATGGTGGCCTACCCTGGAGACACGTCTGGCTGACTGGATCCACAG 549	Db 4	
		Qy 3	
121	430 GTCTTTGGGGCTGCCCTGTGTGCTGAGAAGTGTCAACAAAAATGGAGCCTTTGGTGGGA 489	Db 4	
121	301 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGGAGCCTTTTGGTGGA 360	Ωу з	
Db 61 AAGCTGAGG	370 CAGGTTTCCGACGACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 429	Db 3	
61	241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGGATTCTTT 300	Оу 2	
<b>-</b>	310 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 369	Db 3	
Qy 1 ATGCCGACC	181 TTCTCTGACCTGGCCGCTCAGCTGACGCTGACCCCAGGCTCAGCCCAGCAGCAACGCTTCACC 240	Qy 1	
Query Match Best Local Similarity Matches 531: Consei		Db 21	
ORIGIN			
/5		Db 19	

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TGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG
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91.4%; Pred. No. 3.7e-117;
++vra 0; Mismatches 50;
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AL157542

BO4 bp mRNA linear EST 04-SEP-2003

EFINITION DKEZP761D0816 rl 761 (synonym: hamy2) Homo sapiens cDNA clone

DKEZP761D0816 5', mRNA sequence.

AL157542.1 GI:7057943

EYRORDS

EST.

OURCE Homo sapiens (human)

ORGANISH Homo sapiens (human)

ENTRENCE 1 (bases 1 to 804)

ANDTHORS Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.

TITLE ST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.

Unpublished (1999)

OMMENT MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the

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                             mRNA sequence.
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601590016F1 NIH_MGC_7
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No s1 sequence available.

This clone (DKFZp7610816) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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/mol type="mRNA"
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/dev_stage="adult"
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/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sa.
                                            GI:10214832
             (human)
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Pred. No. 4.1e-111;
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               AGTIGGGGGCTIGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCCTGGAGGAGGCGCGG
                                           AGTGGCGGCTGGGCGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG
                                                                          CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
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323 180

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Email: ogapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.e
plate: LLCM800 row: p column: 04
High quality sequence start: 5
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGGCTGACTTTGTAGGCTAT
ATGGCGACCCCAGCCTCGGCCCCAGACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT
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                                                                                                          Conservative
                                                                                                                                                                                                                                   /clone lib="NIH MGC_7"
/clone lib="NIH MGC_7"
/note="Organ: lung; Vector: pCTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3944307"
/tissue_type="small cell
/cell_line="MGC3"
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'db_xref="taxon:9606"
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'clome lib="NIH MGC 7"
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No. 6.5e-111;
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Hominidae; Homo.
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Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
plate: LLAM9853 row: h column: 07

High quality sequence stop: 650.

High quality sequence stop: 650.
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National Institutes of Health,
Unpublished (1999)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 815)
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                                                                                                                                                                                                     GCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                   GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTT
                                                                                                                                                            GGCTGCTGGAGACGAG-TTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                   TGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGGCCGACCCGCTGCACCAAGCCATGCG
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     CCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTTGGGGGCCTGCCCTGTG
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/lab_host="DH10B (TI phage_resistant)"
/clone_lib="NCI_CGAP_Kid14"
/clone_Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library. | "
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1.1e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
The FANTOM Consortium and the Group Phase I & II Team.
Analysis of the mouse transcri
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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11 days embryo whole body cDNA, RIKEN full-length
, clone:2810435A13 product:Bcl2-like 2, full insert
     transcriptome based
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26 (bases 1 to 854)

S. Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiramoto, K., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shizaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yeshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                         196 ATGGCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 255
  61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-Jul-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIXEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL, http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax:81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                            /protein_id="BAB28740.1"
/db_xref="G1:12850488"
/db_xref="G1:12850488"
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GAALCAESVNKEMEFLVGQVQDWWVAYLETELADWIHSSGGWVRSSQLLLSASLYKVG
                                                                                                                                                                                                                                                                                                              LHGKIGPLMGGWGCAGRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MGD | MGI: 108052)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="unnamed protein product; Bcl2-like 2
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/db_xref="MGI:1902183"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 21 High quality sequence stop: 695. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11526 row: k column: 15
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone lib="NIH MGC 122"
/clone lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: Not1; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
                    primed and directionally cloned (EdoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
(Invitrogen).
                                                                                                                                                                                                                                                                                                     lone="IMAGE:5209862"
Research Genetics
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

DNA Sequencing by: Incyte Genomics, Grant Clone distribution: MGC clone distribution informat

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                        BG298789 792 bp r
602396527F1 NIH_MGC_94 Mus musculus
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
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AMGNNUC:NRDG1-00100-H10-A nrdg1
clone nrdg1-00100-h10 5', mRNA 6
CB578463
CB578463.1 GI:29522504
EST.
                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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Contact: Dan Fitzpatrick
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/mal_type="makNa"
/mb_xref="taxon:10090"
/clone="IMAGE:4511215"
/clone="IMAGE:4511215"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 94"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Rodentia;
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540 bp mRNA linear BST 23-DEC-1999 um74a02.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2300906 5' similar to SW:BCLW MOUSE P70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence.
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wy Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Waterston,B. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Mammalia; |
                                                                                                                           Mus musculus
                                                                                                                                         Mus musculus (house mouse)
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/tissue_type="Dorsal Root Ganglia"
/clone_lib="nrdg1 (10855)"
/note="Vector: psporm1; Site_1: Sall; Site_2: Not1; rat
                                                                                                  Eutheria;
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db_xref="taxon:10116"
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                                                                                   1 to 540)
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Pred. No. 3.2e-93;
0; Mismatches 16
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MGI:1009678
Seq primer: custom primer used
High quality sequence stop: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis Tel: 314 286 1800

Fax: 314 286 1810
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                                                                                /clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/note="Torgan: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTTT] double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]; digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
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/clone="IMAGE:2300906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
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Query Match Best Local Simi Matches 420; Local Similarity 472 361 412 301 352 241 292 181 232 121 172 112 13 ب AGTGGCGGCT CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420 GTCTTTGGGGCTGCCCTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGGAAGGCCCAGCCCGCCGAC ATGGCGACCCCAGCCTCAACCCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGGCTGACTTTGTAGGCTAT CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGGCCGTCTTGTGGCATTCTTT CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAAGGCCCAGCCGCCGAC TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC Conservative 69.5%; 0 Score 403.6; DB 1 Pred. No. 2.8e-92; Mismatches 9 Indels <u>بر</u> Gaps 360 471 411 300 351 240 291 180 231 120 171 60

γŞ	99 V2	Db Qy	Query Mat Best Loca Matches	ORIGIN	1	FEATURES	FEA TIRES	COMMENT	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE	ORGANISM	KEYWORDS	ACCESSION VERSION		DEFINITION	CA391923
121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACCAGTTTGAGACCCGTTTCCGCCGCACC 180	61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGACCCGCCGAC 120	1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60	ch 1 simil 408; C	OR PAROMOTER DEPMENT		Location/Qualiti		Contact: Wistow G	22103460 12107410	Mol. Vis. 8 (4), 205-220 (2002)	sequence tag analysis of human oject: Over 6000 non-redundant	<ol> <li>Wyatt, M.K., Farris, R.N., Beha</li> <li>Smith, D. and Peterson, K.</li> </ol>	Eukaryota; Metazoa; Chordata; Craniata; vercebrata; Eutereostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 626)	sapiens	EST.	CA391923 CA391923.1 GI:24724221	(Un-mormanized, unamprilled): Os nomo saprems cons crome oszocos 5', mRNA sequence.	Human Retinal pigment epithelium/choroid cDNA	727

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595 AGTGGGGCTGGGCGGAGTTCACAGCTCTATA 626	421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATA 452	535 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGACTGGATCCACAGC 594	361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420	475 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 534	7 301 GTCTTTGGGGCTGCCCTGTGTGCTGAAGAAATGAAAAAAAA	415 CAGGTCTCCGATGAACTTTNTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 474	241 CAGGTTTCCGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGGATTCTTT 300	355 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 414	181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240	295 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 354

Search completed: March 29, 2004, 07:28:10 Job time: 2269.1 Becs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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## SUMMARIES

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## ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX022531	RESULT 1
apoptosis-controlling genes Patent: EP 0932674-A 8 04-AUG-1999;	A novel mammalian gene, bcl-w, belongs to the bcl-2 family of	Adams, J.M., Holmgreen, S.P., Cbry, S. and Gibson, L.M.		unclassified.	unidentified	unidentified .	•	AX022531.1 GI:10046127	AX022531	Sequence 8 from Patent EP0932674.	AX022531 581 bp DNA linear PAT 07-SEP-2000		

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FEATURES

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OPERATIONS

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RESULT 2
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unidentified unidentified unclassified.
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                                            AX030819 581 bp
Sequence 8 from Patent W09735971.
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GAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCTGCACCAAGCCATGCGGGCTGCTGGAGAACGAGTTTGAGACCCGTTTCCGCCGCACC
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/mol type="unassigned DN:
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Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., C. Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. bcl-w, a novel member of the bcl-2 family, promotes Oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-JUN-1996) Molecular Biology Unit, The Walter an Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia Location/Qualifiers
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CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                     GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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//bb_xref="GI:1572495"
//db_xref="GI:1572495"
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//translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAMDPLHQ
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GAALCABSVNKEMEPLYGQVQDMYVAYLETRLADWIHSSGGWABFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="promotes
codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:1572494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _line="BaF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; l
Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 560.2; DB 10;
Pred. No. 5e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell survival; Bcl-2 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernard, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Walter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copeland, N.G., and Cory, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell survival
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AF030769
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AUTHORS
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                  polyA_signal
                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 3476)
Ross,A.J. and MacGregor,G.R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 3476)
Ross, A.J., Waymire, K.G., Moss, J.E.,
MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF030769
Mus musculus BCL-W (Bcl-w) mRNA,
AF030769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-OCT-1997) Center University, 1462 Clifton Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcl-w is required for testis homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF030769.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGTGCAGGATTGGATGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTCTGCGGGAAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG
                        3428. .3441
                                                                                                                                        RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                         /translation="matpastpdtralvadfvgyklrQkGyvCGAGpGEGPAADPLHQ
AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                                                                                                                                                                                                                                                                                                                                                                                            83. .170
                                                                                                                                                                                                       /product="BCL-W"
/protein_id="AAB86430.1"
/db_xref="GI:2623250"
                                                                                                                                                                                                                                                                                       179. .760
                                                                                                                                                                                                                                                                                                        /gene="Bcl-w"
/number=3
                                                                                                                                                                                                                                                                                                                                                        /gene="Bcl-w"
/number=2
                                     /note="mRNA destabilization
                                                   356. .3364
/gene="BCl-w"
                                                                                       /number=4
                                                                                                                                                                                                                                                        gene="Bcl-w"
codon_start=1
                                                                                                                                                                                                                                                                                                                                            L71. .610
                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Bcl-w"
/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
     'gene="Bcl-w"
                                                                                                       gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           map="19.5 cM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="C57BL/10J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for Molecular Medicine, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
complete
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                                       element"
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DEFINITION
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AF096291
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ORGANISM
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         2 (bases 1 to 582)
2 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                   1 (bases 1 to 582)

Hammer, S., Skoglosa, Y. and Lindholm, D.

Differential expression of bcl-w and bcl-x messenger developing and adult rat nervous system developing and adult rat nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTTGTAGGCTAT
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus Bcl-w
AF096291
                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF096291.1 GI:3747129
                                                                                                                                                                0366024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGTGCAGGATTGGATGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
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Rodentia;
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/translation="MATPASOPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQ
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AMRAAGDEFETRERTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/mol type="mRNA"
/strain="Sprague-Dawley"
/strain="Sprague-Dawley"
/db_xref="taxon:1016"
/tissue_type="brain"
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Itoh, T., Itoh, A. and Fleasure, D.
Bcl-2-related protein family gene expression
oligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
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Blvd., Philadelphia, PA 19104, USA
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Mammalia; Eutheria;
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Similarity 96.0%;
58; Conservative
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CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTG
                                               AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG
                                                                                       CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC
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/protein_id="AAO64470.1"
/db_xref="GI:32185285"
/db_xref="GI:32185285"
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QRETQVSDELFQGGPNWGRLVAFEVFGAALCAESVNKEMEBLVGQVQDWNVTYLETRL
ADWIHSSGGWAEFTALYGDGALBEARRLREGNWASVRTVLTGAVALGALVTVGAFFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Pred. No. 2.6e-117;
0; Mismatches 23;
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               CAGGTTTTCCGACGACGTTTTCCAAGGGGGCCCCTAACTGGGGCCCGTCTTGTGGCATTCTTT
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                                                                                       TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC
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                                                        TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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Rattus norvegicus BCL-W mRNA,
AY185098
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Itoh,T., Itoh,A. and Pleasure,
Direct Submission
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Bcl-2-related protein family gene expr
cligodendroglial differentiation
J. Neurochem. 85 (6), 1500-1512 (2003)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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vd., Philadelphia, PA 19104, USA
Location/Qualifiers
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                                                                                                        /translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGFGEGPAADFLHQ
ARRAAGDFFETRETSDLAAQLHVTFGSAQQFTGVSDELFQGGPNMGRLVAFFVF
GAALCAESVKEMBEJUGQVQDMYYYLETRLADWIHSSGGMABFTALYGDGALEEAR
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/db_xref="GI:32185281"
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                   93.7%;
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Rodentia;
Score 544.2; DB 10;
Pred. No. 2.1e-117;
0; Mismatches 23;
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Direct Submission
Submitted (22-SEP-2003) Biotechnology, F
Submitted Nei-Pu Hsiang, Pingtung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mis musculus Bcl2-like protein 2 mRNA, complete cds. AY170344
AY170344.2 GI:34857712
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Direct Submission
Submitted (29-OCT-2002) Biotechnology, F
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Mammalia; Eutheria;
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Mus musculus
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93.1%;
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/strain="C57BL"
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/dev_stage="neonatal"
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182...763
                                                                         /codon_statt=1
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RLREGNWASVRTVLTGAVALGALVTVGAPFAYK"
                                                                                                                                                                                                   /note="c98; Bcl2-c98"
                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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Rodentia;
Score 541; DB
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<sub>1</sub>, Taiwan 9
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Guastella, J.
Genes coding for bcl-y a bcl-2 homologue
Patent: US 5789201-A 1 04-AUG-1998;
Location/Qualifiers
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                                                                                 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
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                      AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCTGGGGAAGGCCCAGCCGCCGAC
                                                               ATGGCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT
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                                                                                                                          Conservative
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/organism="unknown"
/mol_type="unassigned
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95.9%;
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                                                                                                                         Score 540.6; DB 6;
Pred. No. 2e-116;
0; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
                                                                                AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
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                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                 Direct Submission

Submitted (03-JUN-1996) Molecular Biology Unit, The Submitted (03-JUN-1996) Molecular Biology Unit, The Silza Hall Institute of Medical Research, PO Royal Hospital, Parkville, Victoria 3050, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
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U59747
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 582)
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1. .582
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Euteleostomi;
; Homo.

540 540

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Adams, J.M.

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KEYWORDS
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ORGANISM
                                JOURNAL
MEDLINE
PUBMED
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AUTHORS
TITLE
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2 (bases 1 to 3542)
Ohara, O., Nagase, T., Kiku
Direct Submission
Submitted (27-AUG-1996) (
1532-3, Yana, Kisarazu, (
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Human mRNA for KIAA0271
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KIAA0271.
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                                                                                          Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y., Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human ger The coding sequences of 80 new genes (KIAA0201-KIAA0280) dec analysis of cDNa clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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gene,
   Osamu Ohara, Kazusa DNA
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complete cds
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                                                Nomura, N
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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1. .3542
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GAALCAES\UKKEMEPLVGQVQEMMVAXLETRLADWIHSSGGMAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/db_xref="taxon:9606"
/clone="HA6752"
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                                                                                                                                                                                      AGTGGCGGCTGGGCCGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAAGGACGCACGG
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/db_xref="G1:10046126"
/db_xref="RMTREMEDI:CAC07880"
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ARRAAGDEFFTRFRTTSDLAAQLHVTTGSAQQRFTGVGSDELFGGGPNGGLVAFFLF
GAALCAES/WKEMBFLYGQOGMYVAYLETRLYDMIHSSGGMAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/db_xref="taxon:32644"
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/db_xref="taxon:32644"
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Patent WO9735971.
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Pred. No. 4e-107;
0; Mismatches 5
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Gaps

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DY 541 GGGGCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579	Db db
AB1 CGTCTGCGGGAAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTG 540	D Sy
NY 421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480	요 성
y 361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420	dd Qy
301	DЬ
241 C 241 C	d V
y 181 TYCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCGAGCG	99
y 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCCGACC 180	B 8
y 61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC 120	db Qy
Y 1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACCTTTGTAGGCTAT 60	g S
Query Match 85.6%; Score 497.4; DB 6; Length 579; Best Local Similarity 91.2%; Pred. No. 2.8e-106; Matches 528; Conservative 0; Mismatches 51; Indels 0; Gaps 0;	
OURCE Unknown.  ORGANISM Unknown.  Unclassified.  U	SOURCE ORG ORG REFER AUT TIT JOU FEATU
RESULT 15 AR020780 AR020780 DEFINITION Sequence 2 from patent US 5789201. ACCESSION AR020780 VERSION AR020780.1 GI:3975395 KEYMORDS	RESULIARO20 ARO20 LOCUS DEFIN ACCES VERSI
y 541 gegecctggtaactgtagggecttttttgctagcaagig 581 	Db Qy
y 481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTG 540	Qу

Search completed: March 29, 2004, 06:11:59 Job time : 2757.26 Becs

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Result
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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   AAX15946
AAV41925
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ABS73617
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ABL32228
ABL32228
AAL32229
                                                                                                   ABX09972
ABL91694
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Million cell updates/sec
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Aax25135 Mouse bcl
Aax25135 Mouse bcl
Aax25135 Mouse bcl
Aab52996 Primary r
Aav28333 Rat bcl-y
Aax15945 CDNA meno bcl
Abx35729 Human bcl
Abx191694 Human bcl
Abb191694 Human bcl
Abx16462 Human bcl
Aax25132 Human bcl
Aax25134 Human bcl
Aax26134 Human bcl
Aax2634 Human bcl
Aax2636 CDNA enco
Aav41925 Nucleotid
Aav59630 Human sch
Abx3617 Human sch
Abx3617 Human sch
Abx3617 Human imm
Abi3229 Human imm
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Mouse bcl-w DNA.

22-APR-1998

(first entry)

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Aaf75960	Aax33182	Aas00247			Abk84766	Aac90810	Aas15189		Aat40079	Aaq81698	Aah43464	Aah48169	Abs13513	Aai05940	Abs39016	Aak13683	Aak39424	32370	82	438	Aba65269
Rat wild-	ase	Bcl-X1-DT		Human bcl	Human cDN	Human Bcl	Human bcl	Bcl-x gen	Bcl-XL ge	Human thy	cDNA clon	Mutant bc	Human gen	Probe #59		Human bra	Human bon	Probe #10	þ		Human foe

## ALIGNMENTS

RESULT 1 AAT96578

AAT96578;

AAT96578 standard; DNA;

581 망

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Cory
                                                        WPI; 1997-489635/45.
P-PSDB; AAW36048.
                                                                                               27-MAR-1996;
                                                                                                                    02-OCT-1997.
                                                                                                                            WO9735971-A1.
                                                                                                                                                                          Mus ap.
                                                                                                                                                                                   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
                                                                                                          27-MAR-1997;
                                                                                    (AMRA-)
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                                                                                    AMRAD OPERATIONS PTY LTD.
                                                                         Adams JM, Gibson LM,
                                                                                               96AU-00008965
                                                                                                          97WO-AU000199
                                                                                                                                         1. .507
/*tag= a
/product= "bcl-w"
/note= "q"
                                                                                                                                                               Location/Qualifiers
                                                                         Holmgreen
                                                                         SP;
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This sequence encodes a novel gene, bol-w, from the mouse bol-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,

Claim 3; Page 50-51; 86pp; English.

diseases.

Nucleic acid encoding inhibit cell survival,

apoptosis related gene e.g. for treatment of

cancer and bcl-w -

used to induce or and degenerative

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Matches 581;
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                                                                                                                   05-JUL-1999
                                                                   Spermatogenesis; animal model; ss
                                                                                                 Mouse bcl-w gene
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                                                                             Bcl-2; mouse;
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Pred. No. 6e-148;
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         AGTGGCGGCTGGGCCGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG
                                                                                                   GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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                                                                             GTCTTTGGGGCTGCCCTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
                                                                                                                           CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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100.0%;

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Score 581; D: Pred. No. 6e-0; Mismatches

6e-148

BG

2

Length 581; Indels

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Gaps

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480

420 360 360

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240 240 180 180 120 120

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The present sequence is described as a derivative of the mouse bol-w gene (see AAX25133) and encodes Bol-w protein (see AAX05533), a pro-survival member of the Bol-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of considering models and genetic sequences useful for inducing or reducing fertility. Of male animals. Methods are provided for the treatment of infertility, cor for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w companies of the used to screen for the substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis or the content of the conte
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BP; 105 A; 164 C; 195 G; 117 T; 0 U; 0
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                                                                                                                                                                                                                       The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl w. Such animals have disorganised seminterous tubules and are determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, can induce infertility for including spermatogenesis in animals, or which
                                                                                                          Query Match
Best Local S
Matches 568
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                                                                                                                                                                              Sequence 581
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     AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGAC
                                       ATGGCGACCCCAGCCTCAACCCCAGACACACGGCTCTAGTGGCTGACTTTGTAGGCTAT
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97.8%;
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11-APR-2002;
19-APR-2002;
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08-MAY-2002;
09-MAY-2002;
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13-MAR-2002;
08-APR-2002;
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10-APR-2002;
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standard; DNA; 582 ВP

(first entry)

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3538.

toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; hepatocyte toxicity modelling; gene; ds drug screening; diagnostic marker;

WO2003065993-A2

2002US-0371134P. 2002US-0371135P. 2002US-0371139P. 2002US-0371413P. 2002US-0373601P. 2002US-0373602P. 2003WO-US003482 2002US-0370248P 2002US-0363534P

2002US-0374139P 2002US-0378370P 2002US-0378652P 2002US-0378653P 2002US-0378655P 2002US-0378665P 2002US-0394230P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises to preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic ceffect, particularly hepatotoxicity, of a test or unknown compound. The ceffect, particularly hepatotoxicity, of a test or unknown compound. The ceffect in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to ceffectify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for cdrug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
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Best Local Similarity
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04-SEP-2002;
28-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 582 BP; 111 A; 157 C; 200 G; 114 T; 0 U; 0 Other;
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                                                                                                                                                     CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                                                                                                                                                        GICTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTG
                                                                                     AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGCCCTGGAGGACGCACGG
                                                                                                                   CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC
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                                                      <u>AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG</u>
                                                                                                                                                                                                                                                                                                                     TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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; 2002US-0407688P.
; 2003US-0442900P.
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Pred. No. 6.1e-138;
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                                                                                                                                                               Query Match
Best Local S
Matches 555
                                                                                                                                                                                                                                                                                                                                               The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding B-cell lymphoma-y protein - useful for recombinant protein for use in treating uncontrolled cell grov
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                                                                                                                                                                                                                                                                     C; 198 G; 113
                                                                                                                                                               Score 540.6; DB 2;
Pred. No. 5.8e-137;
0; Mismatches 24;
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                                                                                                                                                                                                                                                                                                Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite;
        Disclosure; Col 13-16; 26pp; English
                                                                     WPI; 1999-214150/18
P-PSDB; AAW97391.
                                                                                                         Guastella
                                                                                                                                                       23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                   16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding
                                 modulating
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RESULT 7 ABV78153 ID ABV7 XX AC ABV7 XX DT 15-N

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ABV78153;

15-NOV-2002

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The present sequence encodes rat bcl-y protein (Rbcl-y). The specification also describes human bcl-y protein (Rbcl-y) Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y corrections may be used to treat conditions associated with a disruption of CC the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, CC (aspecially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC ell death, aging, spinal cord injuries and amyotrophic lateral sclerosis CC triggers which may or may not be apparent. They may also be used in this CC way to develop cell lines which remain viable in culture for an extended CC period. In contrast, if they act as cell death stimulators, Rbcl-y and CC bloomy be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sercoma and lung cancer) CC and auto/hyperimmune diseases. They may also be used to cause cell death can and hence control, parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 555
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GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                                                               CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG
                                                                                                                     AGTGGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG
                                                                                                                                                                                                                           CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                                                                                                                                             CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC
                                                                                                                                                                                                                                                                                                     GTCTTTGGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
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                                                                                                                                                                                                                                                                     rgoggetigeettgtgtgtgagagtgteaacaaagaaatggageeattggtggga
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Pred. No. 5.8e-137;
0; Mismatches 24;
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Query Match
Best Local S
Matches 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes. e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention
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29-NOV-2001;
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                                                                                CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                           CAGGTCTCCGACGAACTTTTTCAAGGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                                                              CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                             AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
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GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
                          GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
                                                                                                                      TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                  ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT
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; 2001DE-01060151.
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                                                                                                                                                                                                                                                                                                                                                                Score 505.8; DB 6;
Pred. No. 1.7e-127;
0; Mismatches 47;
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Query Match

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                                                        The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonuclectides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; viru protozoacide; gene expression; antisense; tumour; infection; Plasm virus; viroid; anti-GPP; human; HIV; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; human papilloma virus; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 30-31; 100pp; German.
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Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon. λq after

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target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which daRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene a least one oligoribonuclectide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nuclectides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsNNAI. The method is used to inhibit expression of E T

Similarity Conservative BP; 104 A; 156 C; 211 G; 111 T; 0 U; 87.1%; 91.9%; 0; Score 505.8; DB 6; Pred. No. 1.7e-127; Pred. No. 1.70 0; Mismatches 47; Indels 0 Other; Length 0 Gaps

CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACACCCGTTTCCGCCGCACC ATGCCGACCCCAGCCTCAACCCCCAGACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT AGGCTGAGGCAGAAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGGAAGGCCCAGCCGCCGAC GGGGCCCTGGTAACTGTAGGGGCCTTTTTTTGCTAGCAAGTG CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC GCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTG regecegaettcacaectctatacegegacegegccctegaegaegcegeg 581 581 540 60 60 480 480 420 360 360 300 300 240 240 180 180 120 120 420

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Best Local S
Matches 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for inhibiting expression of a target gene (ARL91659-ARL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang
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Plasmodium;
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virus; viroid; cytokine; prion; antisense oligonucleotide;
virucide; protozoacide; antibacterial; ds.
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91.9%;
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Pred. No. 1.7e-127;
D; Mismatches 47;
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                                                                            The present sequence is the human bol-w gene encoding Bol-w protein (see AAY05530), a pro-survival member of the Bol-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w gene or in a gene associated with bol -w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An animal model exhibiting reduced protein associated with Bcl-w.
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                                                 07-JUN-2001; 2001AU-00005527
                                                                07-JUN-2002;
                                                                                 12-DEC-2002
                                                                                                 WO200299090-A1
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                Wang
                                  JOHNSON
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                                                                 2002WO-AU000739
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                 Turner
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Pred. No. 1.2e-126;
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Best Local Simi
Matches 532;
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Novel DNAzyme useful for treating tumors, and for enhancing the sensitivity of malignant or virus infected cells to therapy, con catalytic domain and binding domain contiguous to the catalytic comprises domain. a

Disclosure; Page 44-45; 67pp; English

The invention relates to a DNAzyme which specifically cleaves mRNA transcribed from a member of the bcl-2 gene family. The DNAzymes comprise a catalytic domain, binding domains contiguous with the 5' and 3' end of the catalytic domain, and therefore hybridise with, the two regions immediately flanking the purine residue of the cleavage site within the bcl-2 gene family mRNA, at which DNAzyme-catalysed cleavage is desired. A pharmaceutical composition comprising a DNAzyme of the invention is useful for treating tumours in a subject, and for enhancing the sensitivity of malignant or virus infected cells infected cells to therapy. The DNAzymes are useful in diagnostics, therapeutics, prophylaxis, research agents and in kits. The DNAzymes are also useful for increasing the susceptibility of tumour cells to anti-tumour therapies such as chemotherapy and radiation therapy. This polynucleotide sequence represents a human bcl-2 gene of the invention

Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 U; 0 Other;

Similarity

91.6%;

Length 3542;

717 541 657 597 537 477 417 357 481 421 361 301 241 181 297 237 177 121 13  $\vdash$ GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAGTG AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGACGCACGG CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCCAGCAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGGCCTGGGGAAGGCCCAGCCGCCGAC CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGGCCGTGGCACTG CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCCGCCTTGTAGCCTTCTTT TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGGCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT Conservative Score 502.6; DB 7; Pred. No. 2.1e-126; 0; Mismatches 49; Indels 757 0 540 480 420 360 476 300 416 356 180 296 120 236 60 656 536 240 0

AAT96577 standard; DNA; 583 먉

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Best Local Similarity
Matches 531; Conserv
                                                                                                                                                                                                                                                                         This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding apoptosis related gene bcl-w - used to induce inhibit cell survival, e.g. for treatment of cancer and degenerative
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                                                                                                                                                                                                                                                                 screening
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CAGGTITCCGACGAACTITTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                       CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                               AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCCTGGGCCTGGGGAAGGCCCAGCCGAC
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                                                                          CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
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nilarity 91:4%;
Conservative
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degenerative disease; ss.
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/product= "bcl-w"
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Pred. No. 3.4e-126;
D; Mismatches 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAX25134
                                                                        16-SEP-1997;
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                                                                                                                                                                                 WO9913710-A1
                                                                                                                                                                                                                    Homo sapiens.
                                     (HALL-) HALL INST MEDICAL RES WALTER &
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Adams J,
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                                                                                                            98WO-AU000764
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The present sequence is described as a derivative of the human bol-w gene (see AAX25132) and encodes Bol-w protein (see AAY05532), a pro-survival comember of the Bol-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a conclusion of treatment and to an animal model for the identification of completules and genetic sequences useful for inducing or reducing fertility, of male animals. Methods are provided for the treatment of infertility, cor of male animals. Methods are provided for the treatment of infertility, cor of or reducing fertility, by modulating spermatogenesis. An animal model coarries a mutation is at least one allele of the human or murine bol-w companies of the second to series and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis con animals, or which can induce infertility

Disclosure; Page 36;

52pp; English

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.

1999-243890/20 DB; AAY05532.

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RESULT 15
AAV28334
ID AAV28
XX AAV28
XX AAV28
XX O2-OC
DT 02-OC
DX Human
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Best Local Similarity

Matches 531; Conserv
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/product= "bcl-y"
/note= "No stop c
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Pred. No. 3.4e-126;
0; Mismatches 50;
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XX
PR 23-FEB-1996; 96US-0012201P.

XX
CCCE-) CCCENSYS INC.

XX
Guastella J;

XX
PI Guastella J;

XX
WPI; 1998-446079/38.
PP PSDB; AAW61392.

XX
Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g.

XX
PI cancers.

XX
Claim 3; Column 15/16; 27pp; English.

XX
PS
CC family, components in the cell death pathway. The bcl-2 family have both apoptosic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to creombinant genetic constructs to increase its expression in vivo. Also, cativity category activity category activity category activity category activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to continuous to increase its expression in vivo. Also, cativity category activity category activity category activity category activity category. The recombinant protein may be used to cantisense constructs can be used in disorders where prevention of cell category activity category activity category activity category activity activity category. The recombinant protein may be used to category activity category activity category. The recombinant protein may be used to category activity category activity activity category. The recombinant protein may be used to category activity category activity activity category. The recombinant protein may be used to category activity activity activity activity activity activity.
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XX
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 U; 0 Other;
Query Match 85.6%; Score 497.4; DB 2; Length 579;

Ś 멼 Ś 밁 S Matches lecal 121 528; 6 გ Similarity CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC AGGCTGAGGCAGAAGGGTTATGTCTGTGGGAGCCTGGGGCCTGGGGAAGGCCCCAGCCGCCGAC ATGCCGACCCCAGCCTCAACCCCCAGACACCACGCGCTCTAGTGGCTGACTTTGTAGGCTAT AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC ATGGCGACCCCAGCCTCGGCCCCAGACACACGCGCTCTGGTGGAAGACTTTGTAGGTTAT Conservative 91.2%; Score 497.4; Pred. No. 3.2e 0, 1; DB 2; 3.2e-125; nes 51; Indels 0, Gaps 180 120 120 60 60 0

181

TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC

180 240

CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC

121

541

Job time : 363.378 secs

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Result
No.
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re greater than or equal to the score of the result being printed,
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length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/BCCMB.seq:*

5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-010-147B-23
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US-08-481-448-5
US-08-481-739-1
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TOPOLOGY: botl
MOLECULE TYPE:
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US-08-798-897-1
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Best Local S
Matches 555
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COUNTRY: US
ZIP: 20005
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                                                                                                 555;
                                                                                                                Similarity
    AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTTGGGGCCTGGGGAAGGCCCAGCCGAC
                                 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                        ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCCTGACTTTGTAGGCTAT
                                                                                                93.0%;
ilarity 95.9%;
Conservative
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ALIGNMENTS

#### ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 1483 REFERENCE/DOCKET NUMBER: 1483 REFERENCE/DOCKET NUMBER: 1483 REFERENCE/DOCKET NUMBER: 1483 REFERENCE/DOCKET NUMBER: 1283 REFERENCE/DOCKET NUMBER: 1483 REFERENCE/DOCKET NUMBER: 1483 REFERENCE/DOCKET NUMBER: 1260 REFERENCE/DOCKET NUMBER: 1283 REFERENCE/DOCKET Sequence 1, Application US/08798897 Patent No. 5789201 GENERAL INFORMATION: APPLICANT: Guastella, John TITLE OF INVENTION: Genes Coding TITLE OF INVENTION: Homologue SEQUENCE CHARACTERISTICS: LENGTH: 579 base pairs TYPE: nucleic acid STRANDEDNESS: both COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM FC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA; CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES: APPLICATION NUMBER: US FILING DATE: February CLASSIFICATION: 435 STREET: 1100 New CITY: Washington E: STERNE, KESSLER, GO 1100 New York Avenue, KESSLER, GOLDSTEIN & FOX P.L.L. ork Avenue, N.W., Suite 600 US/08/798,897 ry 11, 1997 Score 540.6; Pred. No. 2.1e 0; Mismatches 1483.0140001 For Bcl-y, a 6; DB 1; 2.le-144; hes 24; # Length 579;

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; Sequence 1, Application; Patent No. 5883229; GENERAL INFORMATION: APPLICANT: Guastel:
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US-08-978-523-1
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ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
124
PRIOR APPLICATION DATA:
127
CLASSIFICATION 1424
ATTORNEY/AGENT INFORMATION:
NAME: ESMONT NUMBER: 13.893
REGISTRATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ESMONT NUMBER: 32.893
 TELEFAX: 20
             REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Genes Coding For TITLE OF INVENTION: Homologue NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L. STREET: 1100 New York Avenue, N.W., Suite 600
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LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
HOLECULE TYPE: CDNA
US-08-978-523-1
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Best Local Similarity
Matches 555; Conserv
                                                                                                                                                                                                                              Sequence 2, Application US/08798897 Patent No. 5789201
                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Guastella,
TITLE OF INVENTION: G
TITLE OF INVENTION: H
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         NUMBER OF SEQUENCES: 5
                                                                                             STREET: 1100 New CITY: Washington
                                                                                                                            ADDRESSEE:
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1100 New York Avenue,
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                                                                                                                                                                     Homologue
                                                                                                                                                                                   Genes Coding
                                                                                                               KESSLER, GOLDSTEIN
ork Avenue, N.W., Su
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For

Вс1-у,

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IN & FOX P.L.L.C. Suite 600

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CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGTTTCCGACGAACITTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGIGGCATTCTTT
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                                          GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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Pred. No. 2.1e-144;
0; Mismatches 24;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-798-897-2
                                                                                  RESULT 4
US-08-978-523-2
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Sequence 2, Application US/089
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes
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Best Local Similarity
Matches 528; Conserv
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
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ilarity 91.2%;
Conservative
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 Coding For Bcl-y,
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Pred. No. 4e-132;
0; Mismatches 51;
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.6%;
Best Local Similarity 91.2%;
Matches 528; Conservative
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION NUMBER: US/08/978,523

FILING DATE: herewith

CLASSIFICATION: 424
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APPLICATION NUMBER: US
FILING DATE: February 1
CLASSIFICATION: 424
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LENGTH: 579 base pairs
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STREET: 1100 New
CITY: Washington
STATE: DC
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STRANDEDNESS: both
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                            AGTGGCGGCTGGGGGACTTCACAGCTCTATACGGGGACGGCGCCCTGGAGGACGCACGG
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                                                              GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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11, 1997
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Pred. No. 4e-132;
0; Mismatches 51;
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-010-1473-23
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US-09-010-147B-23
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 390; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 1098 base pairs
TYPE: nucleic acid
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FILING DATE: 12-NO. 6653445-2002
CLASSIFICATION = (Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: JORACHAN NUMBER: 41,119
REGISTRATION NUMBER: 41,119
REGISTRATION NUMBER: 41,119
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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LOCATION:
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CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180
                                                                                   AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGAC 120
                                                                                                                                                ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
                                                                                                                                                                                              ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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                                                AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
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Pred. No. 2.6e-94;
0; Mismatches 42
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                                                                                      EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,507
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,507
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
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                                                          APPLICATION NUMBER: 60/0
APPLICATION NUMBER: 60/0
TOTAL 1997-05-23
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                                             APPLICATION NUMBER:
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                                                60/047,581
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EARLIER APPLICATION NUMBER: 60/056,662 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,872 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,882 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,637 EARLIER APPLICATION NUMBER: 60/056,903 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,888 EARLIER APPLICATION NUMBER: 60/056,889 EARLIER APPLICATION NUMBER: 60/056,879 EARLIER APPLICATION NUMBER: 60/056,879	EARLIER HAPPLICATION NUMBER: 60/047,582 EARLIER APPLICATION NUMBER: 60/047,596 EARLIER FILING DATE: 1997-05-23 EARLIER HAPLICATION NUMBER: 60/047,612 EARLIER HAPLICATION NUMBER: 60/047,612 EARLIER PILING DATE: 1997-05-23 EARLIER PILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,67 EARLIER PILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,67 EARLIER APPLICATION NUMBER: 60/043,311 EARLIER APPLICATION NUMBER: 60/043,67 EARLIER APPLICATION NUMBER: 60/043,67 EARLIER APPLICATION NUMBER: 60/043,67 EARLIER APPLICATION NUMBER: 60/043,67 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER PILING DATE: 1997-04-11 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/0456,89 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-25 EARLIER FILING	EARLIER FILING DATE: 1997-05-23  EARLIER APPLICATION NUMBER: 60/047,500  EARLIER FILING DATE: 1997-05-23  EARLIER FILING DATE: 1997-05-23  EARLIER FILING DATE: 1997-05-23  EARLIER APPLICATION NUMBER: 60/047,492  EARLIER APPLICATION NUMBER: 60/047,598  EARLIER APPLICATION NUMBER: 60/047,598  EARLIER APPLICATION NUMBER: 60/047,613  EARLIER APPLICATION NUMBER: 60/047,613  EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION UNDEER: 60/056,875 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,887 EARLIER APPLICATION NUMBER: 60/056,908 EARLIER APPLICATION NUMBER: 60/046,908 EARLIER APPLICATION NUMBER: 60/048,964 EARLIER APPLICATION NUMBER: 60/048,964 EARLIER FILING DATE: 1997-06-06 EARLIER APPLICATION NUMBER: 60/057,650 EARLIER APPLICATION NUMBER: 60/056,884 EARLIER APPLICATION NUMBER: 60/056,884	EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,864 EARLIER APPLICATION NUMBER: 60/056,631 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,845 EARLIER APPLICATION NUMBER: 60/056,845 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/047,595 EARLIER APPLICATION NUMBER: 60/047,595 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,586 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,586 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,590 EARLIER APPLICATION NUMBER: 60/047,590 EARLIER APPLICATION NUMBER: 60/047,590 EARLIER APPLICATION NUMBER: 60/047,591 EARLIER APPLICATION NUMBER: 60/047,591 EARLIER APPLICATION NUMBER: 60/047,593 EARLIER APPLICATION NUMBER: 60/043,576 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,576 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/043,670 EARLIER APPLICATION NUMBER: 60/043,670 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,631 EARLIER APPLICATION NUMBER: 60/056,631 EARLIER APPLICATION NUMBER: 60/056,631	ASASASASA

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RESULT 7
US-08-081-448-5
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Best Local S
Matches 389
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                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
                                FILING DATE: 19
CLASSIFICATION:
                                                               APPLICATION NUMBER:
                                                                                                                                                                                           COUNTRY:
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ER APPLICATION NUMBER: 60/057,669
ER FILING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/049,610
ER FILING DATE: 1997-06-13
ER APPLICATION NUMBER: 60/061,060
ER FILING DATE: 1997-10-02
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                                                               US/08/081,448
    Thomas
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Pred. No. 4.1e-94;
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                                                                                                 Version
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                                                                                                                                                                                                        RESULT 8
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENERAL INFORMATION: COMPOSITIONS AND METHODS
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; LOCATION:
US-08-081-448-5
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White
                                                                                                                                                                                          NUMBER OF SEQUENCES:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palance ""
                                                                                                                                 STREET:
                                                                                  ZIP:
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AĞĞAACĞÜTTÜAACCGÜTĞĞTTÜCTĞAĞĞĞĞÇATĞAÇTĞTĞĞÜÇĞ
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RESULT 9
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                                                                                                                         Sequence 1, Application US/08481739
Patent No. 6143291
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 236; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081
FILING DATE: 22-UU-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 101000
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NAME/KEY:
LOCATION:
                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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                                                       STREET:
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TYPE: nucleic acid
STRANDEDNESS: single
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Massachusetts
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Pred. No. 7.1e-29;
0; Mismatches 169;
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Best Local Similarity
Matches 236; Conserv
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INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: US/08/.
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/.
REPLICATION NUMBER: US 08/.
PRILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. (()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
FEATURE:
NAME/KEY: CD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
                                                                                                         GCTGGGCGGACTTCACAGCTCTATACGGGGACGGACGCCTGGAGGACGCACGGCGTCTGC
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                                                                    GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 134.6; DB : Pred. No. 7.1e-29
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Sequence 1, Application US/09167921A
Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.

Nic., Brett F., ef, Brian,

US-09-167-921-1

RESULT 10

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US-09-277-020-39
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CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                      Sequence 39, Applicate Patent No. 6210892
GENERAL INFORMATION:
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Best Local Similarity
Matches 236; Conserv
                                                                          SOFTWARE: PatentIn
SEQ ID NO 39
TYPE: DNA
ORGANISM: Homo :
-09-277-020-39
                                                                                                            APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER FILING DATE: 1998-10-07
NUMBER: OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
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ORGANISM: Homo:
FEATURE:
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TITLE OF INVENTION: Antisense Modulation of bcl-x
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                                                             LENGTH: 926
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Pred. No. 7.1e-29;
0; Mismatches 169;
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                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1994-07-26
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                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antisense Modulation of FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-03-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6214986 GENERAL INFORMATION:
                                                                               Query Match
Best Local
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Best Local
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APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
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                                                                                Similarity
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AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG
                             accaaeccareceeecrecresaeaceaerrreaeacceerrreceececaecrrerere
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                                                                                  23.2%;
58.3%;
                                                                 0,
                                                               Score 134.6; DB 3;
Pred. No. 7.1e-29;
0; Mismatches 169;
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Pred. No. 7.1
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-461-511A-6
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US-08-461-511A-6
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Query Match
Best Local Similarity
Matches 236; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-7un-1995
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARCD:179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEPAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTG
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STATE: Texas
COUNTRY: United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAGGGCAACTGGGCATGAGTGACCACAGTGGTGACGGGGGCCG 532
                                                                                                                                                LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                          NAME/KEY:
                                                                                                                                      TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
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                                                                                            CDS
135..836
                  23.2%;
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    Score 134.6; DB 4;
Pred. No. 7.1e-29;
0; Mismatches 169;
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US-09-271-014A-5
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Best Local :
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TYPE: DNA
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FEATURE:
NAME/KEY: CDS
LOCATION: (135)..(836)
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Local Similarity 58.3%;
les 236; Conservation
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                                                         GGGAGGGCAACTGGGCATGAGTGACAGTGGTGACGGGGCCG
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Sequence 5, Application US/09271014A Patent No. 6395510 FILE REFERENCE: ARCD:316
CURRENT APPLICATION NUMBER: US/09/271,014A
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 10 APPLICANT: THOMPSON, CRAIG B.
APPLICANT: BOISE, LAWRENCE H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS

454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGCATTCAGTG 128 ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTG TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTG AGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGCG GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG севствесствтететваванствтельная в поставов 247 633 367 573 307 513 453 187

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Score 134.6; DB 4; Pred. No. 7.1e-29; 0; Mismatches 169;

Indels Length

Gaps

926; 0;

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; LIBRARY: GENBAN
; CLONE: g510900
US-09-023-655-1430
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US-09-023-655-1430
                                                                                                                                     Query Match
Best Local Sim
Matches 236;
                                                                                                                                                                                                                                                                                                         TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPB: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EXITAGE DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHAN: (650) 845-4166
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STREET: 31/-
CITY: PALO ALTO
CTATE: CALIFORNIA
"TSA
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ADDRESSEE: INCYTE PHARMACEUTICALS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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Similarity 58.3%;
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                                                                  AGCAAGCGCTGAGGGAGGCAGGCGACGACTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                               ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTTCCGCCGCACCTTCTCTG 187
ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                         ACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTT 247
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                                                                                                                                   Score 134.6; DB 4;
Pred. No. 7.1e-29;
0; Mismatches 169;
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  AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG
                                      GGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCG 532
                                                                          GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCCC
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Search completed: March 29, 2004, 07:30:35 Job time: 78.3686 secs

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Result
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Maximum DB
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Maximum Match 100%
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                               Database
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
3: sp_fungi:*
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 1 MATPASTPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_phage:*
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O88996 rattus norv
Q8ts60 rattus norv
Q8ts14 mus musculu
Q9cyw5 mus musculu
Q9cyw5 mus musculu
Q9myw4 oryctolagus
O35844 mus musculu
Q8sq42 felis silve
Q9n1A2 sus scrofa
Q9nz87 ovis aries
Q8mz87 ovis aries
Q8mz87 auttus norv
Q7tsnB rattus norv
Q7tsnB rattus norv
Q9bd45 bos taurus
Q9n35 mus musculu
Q90298 brachydanio
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54 suberite	Q9N754	ហ	۳	.4	148.5	ິບາ
43 fe	Q8SQ43	σ	192	14.8	149	4,
b3 cervus e	Q8MJB3	o	67	5		Ü
Q9jkl3 rattus norv	Q9JKL3	11	7	<u>ب</u>	154	ັນ
Q8wz49 homo sapien	Q8WZ49	4	7	5	154	Ë
2 mus	Q8K3J2	11	173	57	156.5	ö
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Q9rlb3 rattu	Q9R1B3		58	6	162	ã
Q967d2 geodi	Q967D2		w	ა	163	7
Q9h1r5 homo s	Q9H1R5		125		168.5	ñ
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Q98u13 xen	Q98U13		N	7.	172.5	4
Q9i9n4 brachyda	Q9I9N4		Ø	7.	174.5	ω
Q8c264 mus	Q8C264		0		182	ถ
Q9wuis ratt	21UW6Ö		7	8	185	Ξ
Q9jk59 rattus	Q9JK59		O	8	187	ö
Q8uwj1 gall	Q8UWJ1		89	٩	296	ΰ
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Q99n36 mus	Q99N36		$\mathbf{r}$	٠	347	7
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Q9h1r6 homo sapien	Q9H1R6	4	œ	٥,	72	ũ
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mus.	Q9QWX2	11	œ	.7	74	ĩ
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InterPro; IPR000012; Bc12_BH4. InterPro; IPR002475; BC12_Family. Pfam; PF00492; Bc1-2; 1. Pfam; PF00492; Bc1-2; 1. Pfam; PF02180; BH4; 1.	15529; F:apc 06915; P:apc	P; Q07817; IMAZ.	EMBL; AF096291; AAC64200.1;	J. Neurochem. 85:1500-1512(2003).	"Bcl-2-related protein family gene expression during oligodendroglial	ed=12787069; sure D.;	prague-Daw	SEQUENCE FROM N.A.		developing and adult rat nervous system."; Neuroscience 91:673-684(1999).	ial expression of bcl-w	Hamner S., Skoglosa Y., Lindholm D.;	MEDLINE=99292146; PubMed=10366024;	STRAIN-Sprague-Dawley: TISSUE-Brain:		I_TaxID=10116;	a; Rodentia; Sciurognathi; Muridae;	<pre>ractus norvegicus (rac). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>		Bc1-w.		, Created)		O88996 PRELIMINARY; PRT; 193 AA.	SULT 1

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WART; SMO0265; B44; 1.

PROSITE; PS50066; BCL2 FAMILY; 1.

R PROSITE; PS01080; BH1; 1.

R PROSITE; PS01269; BH2; 1.

PROSITE; PS01269; BH4 1; 1.

DR PROSITE; PS01260; BH4 2; 1.

DR PROSITE; PS0063; BH4 2; 1.

OR PROSITE; PS0063; BH4 2; 1.

CROUENCE 193 AA; 20820 MW; 3
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Best Local Sim
Matches 192;
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Best Local Sim
Matches 192;
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Q7TS60;
01-OCT-2003
01-OCT-2003
01-OCT-2003
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STRAIN-Sprague-Dawley;
MEDLINE=22672518; PubMed=12787069;
Itoh T., Itoh A., Pleasure D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Bcl-2-related protein family gene differentiation.";
J. Neurochem. 85:1500-1512(2003).
EMBL; AY185100; AA064470.1;
SEQUENCE 219 AA; 23720 MW; 30E3
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Mammalia; Eutheria; Rodentia;
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                                                                                                                              QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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Pred. No. 3.
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Q8CGL4;
01-MAR-2003 (TIEMBLIE). 2
01-MAR-2003 (TIEMBLIE). 2
01-QCT-2003 (TIEMBLIE). 2
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Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
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Q9CYW5;
01-JUN-2001
01-JUN-2001
01-JUN-2003
BC12-like 2.
                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2002) to the EM EMBL; AY170344; AA013177.1; -. MGD; MGI:108052; BC1212.
                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                          BCL2L2
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STRAIN=C57BL; TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                    GALVTVGAFFAYK
                                                                                                                                                                                                                                                                                                                                                                                                                                             GALVIVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQDWMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSHLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
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                                                                                                                                                                                                 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Chordata;
; Rodentia;
                                                                                    Chordata;
Rodentia;
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he EMBL/GenBank/DDBJ dat
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Last annotation update)
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 965; DB 11;
Pred. No. 1.4e-77;
                                                                                    Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                        Vertebrata; Euteleostomi;
chi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Embryo.

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Best Local Sim
Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BL1; 1.
PROSITE; PS01080; BH1; 1
PROSITE; PS01180; BH4 1;
PROSITE; PS50063; BH4 2;
                                                                                                                                                          Q8CFR2;
Q8CFR2;
01-MAR-2003
01-MAR-2003
01-OCT-2003
Bcl2-like 2.
                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016329; F:apoptosis regulator activity; GO; GO:0006915; P:apoptosis; IEA. InterPro; IPR000712; Bc12 BH. InterPro; IPR0003093; Bc12 BH4. InterPro; IPR0003093; Bc12 BH4. InterPro; IPR0002475; BC12 family. Pfam; PF00452; Bc1-2; 1.
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999
999
SEQUENCE FROM N.A.
TISSUE=Eye;
Strausberg R.;
                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL, AKO13244; BAB28740.1; -.
HSSP; Q07817; 1MAZ.
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                                                                                                                                                                                                                                                                                                                                           QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150
                                                                                                                                                                                                                                                                                                                                                                 QVQDWMVAYLETRLADWIHSSGGWAEFTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                         Chordata;
Rodentia;
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96.7%;
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Last annotation updat
                                                                                                                                                                                                                 Created)
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Pred. No. 2.3e-60;
1; Mismatches 4;
                                                                                         Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E2D4C3F79528E9D7 CRC64;
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Best Local S
Matches 145
          TIGRFAMM; TIGR00865; bcl-2; 1.
PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4 1; 1.
PROSITE; PS05063; BH4 2; 1.
                                                                                                 InterPro; IPR003093; Bcl2_BH4.
InterPro; IPR002475; BCL2_family.
InterPro; IPR004752; Bcl2_reg.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00355; BH4; 1.
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01-OCT-2000
01-JUN-2003
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PROSITE; PS01080; BC12 FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01260; BH4 1; 1.

PROSITE; PS50063; BH4 2; 1.

PROSITE; PS50063; BH4 2; 1.

SEQUENCE 178 AA; 19119 MW; E2
                                                                                                                                                                                                                                                                       Knott J.C., Robertson L., James E.R.;
"Rabbit Bcl-X.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GG; GO:0016329; F:apoptosis regulator GG; GO:0006915; P:apoptosis; IEA. InterPro; IPR000712; Bc12_BH .
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR002475; BC12_family.
                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
InterPro; IPR000712; Bc12_BH.
                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus
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                                                                                                                                                                                                                                              EMBL; AY005131; AAF88137.1;
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                            cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.3%;
96.7%;
 25986 MW;
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Last
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Pred. No. 2.3e-60;
                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; a; Leporidae; Oryctolagus.
 12F0F30344D53F93 CRC64;
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                                                                                                                                                                                                                                                                                                E.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                       sequence up
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                                                                     Query Match
Best Local S
Matches 94
                                                                                                                                                                                                      EMBL; U51278; AAC53459.; -.

R HSSP; P53563; 1AF3.

R MGD; MGI:88139; Bc121.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016329; F:apoptosis regulator activity; IE2

R GO; GO:0016329; F:apoptosis; IEA.

R GO; GO:0016329; F:apoptosis; IEA.

R InterPro; IPR000712; Bc12_BH4.

R InterPro; IPR003093; Bc12_BH4.

R InterPro; IPR003093; Bc12_Family.

R InterPro; IPR004775; BC12_Family.

R InterPro; IPR004775; BC12_Family.

R InterPro; IPR004775; BC12_Teg.

R Ffam; PF00452; BC1-2; 1.

R SYART; SM00337; BC1, 1.

R SYART; SM00337; BC1, 1.

R PFAMS; TIGR00865; BC1, 2; 1.

R PROSITE; PS01080; BH1; 1.

R PROSITE; PS01080; BH1; 1.
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Best Local Similarity
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01-JAN-1998
01-JAN-1998
01-JUN-2003
                                                                                                                                         PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.; "A novel Bel-x isoform connected to apoptosis in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunity 7:629-639(1997).
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                                                                                                                                      ; PS01259; BH3; 1.
; PS01260; BH4_1; 1.
; PS50063; BH4_2; 1.
E 233 AA; 26033 NW
                                                                                       Similarity
                                     RALVADEVGYKLROKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGATGHSSSLDAREVI PMTAVKQALREAGDEFELRYRRAFSDLTSQLHI TPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
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(TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.6%; llarity 42.0%; Conservative 22
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Thymus
                                                                                       43.2%;
                                                                                                                                         26033 MW;
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05,
24,
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%; Pred. No. 5.9e
22; Mismatches
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Last sequence update)
Last annotation update)
                                                                                       Score 435.5;
Pred. No. 1.3
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                                                                       Mismatches
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                                                                                                       Length
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                                                                                                           233;
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Best Local S
Matches 97
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01-JUN-2002 (TrE
01-JUN-2002 (TrE
01-JUN-2003 (TrE
Bcl-x1 protein.
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                                                                                                                QVSDELFQGGDNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHS
                                                                                                                                                             NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                       NGGWDTFVELYGNNAAAESRK--
                                                       SGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                       QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE
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PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS05063; BH4 2; 1.
SEQUENCE 233 AA; 26017 NW; CD17
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00452; Bc1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagafuchi S., Sano J., Kano R., Hasegawa A.;
"Moleculer cloning of feline Bcl-2 family.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AB080951; BAB85856.2;
-GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator activity
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  TIGRFAMs; TIGR00865;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000712; Bc12_BH.
InterPro; IPR003093; Bc12_BH4.
InterPro; IPR002475; BC12_Edmily.
InterPro; IPR004725; Bc12_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
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                                                                                                                                             Similarity
CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
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                                                                                       RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEFWIQE
                                                     RELVVDFLSYKLSOKGYSWSRFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                             Conservative
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                                                                                                                                               42.9%;
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21,
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Last seq
Last ann
                                                                                                                             23;
                                                                                                                          Score 432.5; DB 6
Pred. No. 2.5e-30;
3; Mismatches 58
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; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                      CD17F24FE9D47BC9 CRC64;
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                                                                                                                                                                  DB 6;
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                                                                                                                            Gaps
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Best Local S
Matches 94
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InterPro; IPR003093; Bc12_BH.
InterPro; IPR003093; Bc12_Family.
InterPro; IPR004725; Bc12_reg.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BCL; 1.
SMART; SM00365; BH4; 1.
SMART; SM00265; BH4; 1.
TIGRFAMS; TIGR00865; bc1-2; 1.
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Q9N1A2;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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01-OCT-2000 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
Anti-apoptotic regulator
                                                               01-OCT-2000
01-JUN-2003
                                                                                                        Q9MZS7;
01-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q07817; 1MAZ.
GC; GC:0016020; C::membrane; IEA.
GC; GC:0016329; F:apoptosis regulator
GC; GC:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee T.L., Canty J.M.;
"PCR Cloning of a Porcine bcl-:
"PCR (DEC-1999) to the EM
Submitted (DEC-1999) to the EM
EMBL; AF216205; AAF33212.1; -.
                     Ovis aries
                                                                                                                                                  Q9MZS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
  Eukaryota;
                                           Bcl-x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart;
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E; PS50062; BCL2 FAMILY; 1.

E; PS01080; BH; 1.

E; PS01258; BH2; 1.

E; PS01258; BH3; 1.

E; PS01260; BH4 1; 1.

E; PS01260; BH4 1; 1.
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                                                                                                                                                                                                                                                        NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                           QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEFWIQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                     protein.
                                                          ) (TrEMBLrel.
) (TrEMBLrel.
3 (TrEMBLrel.
  Metazoa;
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                                                                                                                                                  PRELIMINARY;
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  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26047 MW;
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15, Last
24, Last
27 Bcl~xL.
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15,
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Last seq
Last ann
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EMBL/GenBank/DDBJ datab
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  Craniata;
                                                                                                                                                  PRT;
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  Vertebrata;
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  Euteleostomi;
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RRRRR ROOCOG DITT

Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus

Mus musculus (Mouse) B-cell leukemia/lymphoma

the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";

on functional

Team;

annotation

Of.

STRAIN=C57BL/6J; TISSUE=Body; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,

SEQUENCE FROM N.A. NCBI\_TaxID=10090; BCL2.

Q8BQK4 Q8BQK4; 01-MAR-2003 01-MAR-2003 01-OCT-2003

PRELIMINARY;

236

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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

23, 25, 25,

Last sequence update)
Last annotation updat

update)

Created)

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RESULT 11
Q8BQK4
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Best Local :
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PROSITE; PS50062; BCL2 FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4-1; 1.
PROSITE; PS01260; BH4-1; 1.
PROSITE; PS01260; BH4-2; 1.
SEQUENCE 233 AA; 26134 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000712; I
Interpro; IPR003093; E
Interpro; IPR002475; E
Interpro; IPR004725; E
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Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murray J.F., Dong Y.B., Leigh A.J., "Bcl-x in the sheep ovary."; Submitted (JUL-1999) to the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0016329; F:apoptosis regulator
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00337; BCL;
SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P53563; 1AF3.
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                                                                          142
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                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                   NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                          RALVADFVGYKLROKGY-----
                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWVVAYLETRLADWIHSS
                                                                                                                                                                          D------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTFGSAQQRFTQ
                                                                                                                                                                                                  RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV
                                                                                                   VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN
                                                  GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                         GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Bcl2_BH4.
; BCL2_family.
; Bcl2_reg.
                                                                                                                                                                                                                                                              42.5%;
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                                                                                                                                                                                                                                                    23;
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Pred. No. 5.6e-30)
                                                                                                                                                                                                                                                                                                   012BFA1382762915 CRC64;
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RESULT 12
Q7TSN8
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Best Local S
Matches 87
                                           Best Loc
Matches
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GO; GO:00058189; F:apoptosis inhibitor ac
GO; GO:0005815; F:protein binding; IPI.
GO; GO:0005915; P:apoptosis; IDA.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR003093; Bcl2 Family.
InterPro; IPR004725; Bcl2 reg.
Pfam; PF00452; Bcl2 reg.
Pfam; PF00452; Bcl2 reg.
Pfam; PF00105; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00337; BCL; 1.
PROSITE; PS01086; BH4; 1.
PROSITE; PS01080; BH4; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH2; 1.
PROSITE; PS01080; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4 1; 1.
                                                                                                                                                                                                                      Q7TSN8
Q7TSN8;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
                                                                                  Tanaka T., Nangaku M.;
"Rat Bc12-like protein.";
"Rat Bc12-like protein.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF512835; AAA947159.1; -.
SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
MGD; GO
GO; GO
                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                           Bcl2-like protein.
                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                    NCBI_TaxID=10116;
                                                      Local
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AK049473; BAC33767.1;
                       9
                                            l Similarity
87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                       DTRALVADFVGYKLRQKGYVCGAG-----
                                                                                                                                                                                                                                                                                                                  GGWDAFVELYG----PSMRELFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                       GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                            VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                               VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                     SPLRPLVATTGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                                                                                                                                                                       -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNREIVMKYIHYKLSORGYEWDÄGDADAAPLGAAPTPGIFSFOPESNPMPAVHRDMAART
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    DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHRDMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA;
                                            Conservative
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                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                     40.8%;
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                                       Score 412; ub --
pred. No. 1.6e-28;
                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
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Pred. No. 1.6e-
34; Mismatches
                                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                              Length 236;
                                            Indels
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Query Match
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01-JUN-2001 (TrEMBLrel. 17
01-JUN-2001 (TrEMBLrel. 17
01-JUN-2003 (TREMBLrel. 24
Anti-apoptotic regulator B
Bos taurus (Bovine).
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Q7TS61;
01-OCT-2003
01-OCT-2003
01-OCT-2003
SEQUENCE FROM N.A.
Amills M., Bouzat J;
Amills M., Bouzat J;
"Characterization of the bovine bcl-xL gene and rela
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databa
EMBL; AF245488; AAK31307.1; -.
EMBL; AF245489; AAK31308.1; -.
HSSP; Q07817; 1MZ.
GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=22672518; PubMed=12787069;
Itoh T., Itoh A., Pleasure D.;
                                                                                                                                                                          Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiation.";
J. Neurochem. 85:1500-1512(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Bcl-2-related protein family gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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NCE 79 AA; 8602 MW;
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Rodentia;
                                                                                                                                                                                                                                                                                     17, Created)
17, Last sequence update)
24, Last annotation updat
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1-xL (Fragment).
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Last annotation updat
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BJ databases
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SO THE CORRESPONDENCE OF THE CORRESPONDENCE

PROSITE;
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SEQUENCE

180

PS01259; BH3; 1.

InterPro; IPR000712; Bcl2\_BH.
InterPro; IPR002475; BcL2\_family.
Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BcL; 1.
PROSITE; PS50062; BcL2\_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.

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SOURCE BEAUTIFIED BRADER RECORDED TO THE PROPERTY OF THE PROPE
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                                                                                   Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                  InterPro; IPR000712; Bcl2_BH.
InterPro; IPR002475; Bcl2_family.
InterPro; IPR002475; Bcl2_reg.
Pfam; PF00452; Bcl2_reg.
ITGRPAMs; TIGR00865; bcl-2; 1.
PROSITE; PS01062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH2; 1.
PROSITE; PS01258; BH3; 1.
PROSITE; PS01258; BH3; 1.
PROSITE; PS01259; BH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang X.-F., Cantor H.;
"Novel cDNA structure and genomic organization of apoptosis regulatory gene Bcl-x-gamma.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133282; AAK15455.1; -.
EMBL; AF133281; AAK15455.1; JOINED.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SvJ;
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GO:0016329; F:apoptosis regulator activity; IEA.
GO:0006915; P:apoptosis; IEA.
44
QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG
                                                                                        Conservative
                                                                                                                                39.7%;
53.5%;
                                                                                   19;
                                                                                   Score 401; DB 11; Length 217; Pred. No. 1.4e-27; 9; Mismatches 45; Indels
                                                                                                                                                                                                                                                           3B5A4E809A7DEF18 CRC64;
                                                                                   <u>۵</u>
                                                                                   Gaps
    103
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RESULT 15 Q99N35

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104 AALCAESVNKEMEPLYGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163

GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ

157

44 QAMRAAGDEFETRFRRTFSDLAAQLHVTFGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103

QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG

97

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38

Query Match Best Local Simi Matches 76.;

h 39.7%; Score 401; DB 6; Length 18 Similarity 53.5%; Pred. No. 1.1e-27; 76; Conservative 19; Mismatches 45; Indels

Length 180;

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Gaps

180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;

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158 164

ERFNRWFLTGMTVAGVVLLGSL 179 E--GNWASVRTVLTGAVALGAL 183

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192
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                       164 E--GNWASVRTVLTGAVALGAL 183
                                              132 GALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQ 191
                                                                                              72
                                                                                             ERFNRWFLTGMTVAGVVLLGSL
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Search completed: March 25, 2004, 15:44:27 Job time: 37 secs

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Maximum DB
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Perfect score:
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Maximum Match 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query
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Compugen Ltd.
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## ALIGNMENTS

RESULT

I49056

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-233 <KAMN A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623 C;Superfamily: bcl apoptosis regulator, inhibitory type A;Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648 R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. submitted to the EMBL Data Library, November 1994 A;Description: IL-5 inhibits anti-igM-induced apoptosis in an immature B control of the Market State of the C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence revision 02-Uul-1996 #text\_change 28-Jul-2003
C;Accession: I49056; S52866
R;Fang, W,; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T l;A;Accession: I49056; MUID:95052804; PMID:7963517
A;Accession: I49056
A;Status: preliminary; translated from GB/EMBL/DDBJ 밁 S δ 밁 Ş 밁 Ś A; Molecule type: mRNA A; Residues: 1-233 < RES> В A; Accession: S52866 Matches Best Local Query Match 141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183 125 81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNXEMEPLVGQVQDWWVAYLETRLADWIHS 140 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 93; σ Similarity NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229 RELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE Conservative 41.3%; 42.5%; 22; Mismatches Score 428.5; DB 2 Pred. No. 2.2e-32; DB 2; Length 233; 57; Indels 53; Gaps T lymphocytes cell 80 124 65 8 4 line

RESULT B47537

apoptosis regulator bcl-xL - human N;Alternate names: bcl-2-related protein

N;Contains: apoptosis regulator bcl-xS

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R;Boise, L.H.; Gonzalez-Garcia, M.; rublema, C.L., 2007.608, 193
Cell 74, 597-608, 193
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of A;Reference number: A47537; MUID:93364977; PMID:8358789
                                                                                                                                                                                                    A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-233 <MIO-
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177
A;Cross----- embryonic; brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:G623236; PIDN:CAA80662.1;
                                                                                                                                                                                                                                                                                                                    A; Reference number: S51761
A; Accession: S51761
                                                                                                                                                                                                                                                                                                                                                             R;Michaelidis, T.M. submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; A;Accession: C47537
                                                                                         A; Note: smaller form due to splicing
                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2003
;Accession: B47537; C47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Status: nucleic acid sequence
                                                                                                                        ;Molecule type: DNA;Residues: 1-125,189-233 <MI2>;Cross-references: EMBL:X82537; NID:g607176;
                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Rattus norvegicus
;Date: 07-May-1995 #sequence
;Accession: S51761; S51762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
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                                                                                                             Experimental source:
                                     Superfamily:
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                                     apoptosis regulator,
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                                                                                                               embryonic; brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (Norway
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_revision 01-Sep-1995 #text_change 28-Jul-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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Pred. No. 2.8e-32;
3; Mismatches 59;
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                                     inhibitory type
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                                                                                                                                  PIDN: CAA57887.1;
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R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C. Biochim. Biophys. Acta 1132, 109-113, 1992
A;Title: Molecular cloning and DNA sequence analysis of A;Reference number: S24390; MUID:92379084; PMID:1511008
A;Status: preliminary
                                                                                                                                                                                         RESULT 5
S24390
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Query Match

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Score

424.5;

BG ν •-

Length

J.C.

28-Jul-2003

CDNA

encoding

chicken homologue

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transferming protein (bc1-2-alpha) - chicken

C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #text_change 28-.
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-.
C;Accession: A37332; 835453
R;Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bc1-2 gene: 4,Reference number: A37332; MUID:92375724; PMID:1508712
A;Reference number: A37332
A;Residues: 1-233 <EGUP
transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 189/3
C;Superfamily: b
C;Keywords: mito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: bcl apoptosis regulator, Keywords: mitochondrion; transforming
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Best Local :
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                                                                                                                                                     DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
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2; Mismatches 56;
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transforming protein bcl-2, splice form alpha - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Cate: 31-Dec-1988 #sequence revision 07-Jun-1996 #text_change 28-Jul-2003
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
C;Guchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression A;Accession: C37332; MUID:92375724; PMID:1508712
A;Accession: C37332
                            A;Kesidues: 1-58,'T',60-116,'R',118-239 <CLB>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PII
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wri
Oncogene Res. 2, 263-275, 1988
A;Title: Consequences of the t(14;18) chromosomal translocation
A;Reference number: A27622; MUID:88217344; PMID:3285301
A;Accession: A27622
A;Molecula term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: this report is a correction R;Tsujimoto, Y.; Croce, C.M.
R;Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein A;Reference number: A29409; MUID:86259760; PMID:3523487
A;Reference number: A29409; MUID:86259760; PMID:3523487
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A;Residues: 1-232 <CAZ>
A;Cross-references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; C;Superfamily: bcl apoptosis regulator, inhibitory type C;Keywords: mitochondrion; transmembrane protein
                                                                                                                                                                                                                               A;Title: Cloning and structural analysis of cDNAs for bcl-2
A;Reference number: A24428; MUID:87002488; PMID:2875799
A;Accession: A24428
                                                                                                                                                                                                                                                                                                  R;Cleary, M.L.; Smith, S.D.; Sklar, Cell 47, 19-28, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-95, 'A', '97-109, 'G', 111-236, 'S', 238-239 <TSU's
A; Residues: 1-95, 'A', '97-109, 'G', 111-236, 'PIDN: AAA51813.1; PI
A; Cross-references: GB: M13994; NID: 9179366; PIDN: AAA51813.1; PI
A; Note: this sequence has been corrected in reference A37332
A; Note: this sequence has been corrected in reference A37332
R; Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett,
EMBO J. 7, 123-131, 198
A; Title: Alternative promoters and exons, somatic mutation and
A; Reference number: S02452; MUID: 88196071; PMID: 2834197
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A; Residues: 1-232 < CA
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A; Residues: 1-239 <SET>
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A; Residues: 1-239 < EGU >
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mRNA
,'T',60-239
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37.7%; Pred. No. 4.9e-31;
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Wright, J.J.;
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<HUA>

142

VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN

189

141

VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS

GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK

- PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK

190

GGWDAFVELYG--

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RiTilly, U.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: 153295; MUID:95129487; PMID:7828336
A;Accession: I67432
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
C;Accession: 167432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl apoptosis regulator, inhibitory type C;Keywords: alternative splicing; apoptosis; B-cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A; Note: the sequence was determined from the germline;
C; Comment: Constitutive expression of BCL2 following t
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 18q21.3-18q21.
C;Function:
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                                                                                                                                                                                                                                            A;Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; C;Superfamily: bcl apoptosis regulator, inhibitory type
                                                                                                                                                                                                                                                                                         A; Residues: 1-236 < RES >
                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                        ----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                   DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART
                                                                                                                       DTRALVADFVGYKLRQKGY-----
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37.0%;
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Pred. No. 8.8e-31;
                                                                                                                                                                                    Score 411;
Pred. No. 9
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A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4167-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vai
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tayMolecule type: DNA
A;Residues: 1-33, 'E',34-220, 'AL',223-236 <EGU'>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane I
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TVMSA1
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C;Date: 31-Dec-1988 #sequenc
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated A,Molecule type: mRNA A,Residues: 1-236 <RES>
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A;Title: Cloning and sequencing of a cDNA encoding the rat
A;Reference number: 153744; MUID:94193015; PMID:8144041
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1)98 #sequence_revision 29
C;Accession: I53744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Negrini, M.; Silini, E.;
Cell 49, 455-463, 1987
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A; Residues: 1-236 < NEG>
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  Conservative
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                 40.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kozak, C.; Tsujimoto, Y.; Croce,
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Pred. No. 2.8e-30;
Score 405; DB 1;
Pred. No. 3.5e-30;
3; Mismatches 61
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  61;
                                      Length 236;
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R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: 153295; MUID:95129487; PMID:7828536
A;Accession: 167431
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C;Superfamily: bcl apoptosis regulator, inhibitory type
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A;Residues: 1-233 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                      QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHS 140
                                                                                                                                                                           CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                   RALVADFVGYKLRQKGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
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NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                  QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                           NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
                                                                                                                                                                                                                RELVVDFLSYKLSOKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                     40.1%;
                                                                                                                                                                                                                                                                                     22; Mismatches
                                                                                                                                                                                                                                                                                                         Score 404.5;
Pred. No. 3.8
                                                                                                                                                                                                                                                                                                       3.8e-30;
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                                   183
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B-cell lymphoma 2 protein - Chinese hamster C;Species: Cricetulus griseus (Chinese hamst C;Date: 17-Nov-2000 #sequence_revision 17-NC C;Accession: JC7383
                                                                                                                                                         R;Tomicic, M.T.; Christmann, M.; Kaina, B. Biochem. Biophys. Res. Commun. 275, 899-903, A;Title: Cloning and functional analysis of
A;Cross-references: GB:AJ271720
C;Comment: This protein has ant
C;Genetics:
                                                        A; Molecule type: mRNA
A; Residues: 1-236 < TOM >
                                                                                               A; Accession: JC7383
                                                                                                                      A; Contents: Ovary
                                                                                                                                      A; Reference number: JC7383
                  has anti-apoptotic
                                                                                                                                                                                                                                            hamster)
17-Nov-2000
                    function,
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                    and
                  supports
                                                                                                                                                               the
                                                                                                                                                               hamster
                    cell
                                                                                                                                                               Bc1-2
                      survival
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protein

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RESULT 13

I49057

bcl-x transmembrane deleted - mouse
bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 28-Jul-2003
C;Accession: I49057
R;Fang, W.; Rivard, U.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T h.Peference number: I49055; MUID:95052604; PMID:7963517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
A47537
A47537
Apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Species: 03-May-1994 #text_change 28-Jul-2003
C;Jate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 28-Jul-2003
C;Accession: A47537
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Cell 74, 597-608, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
C;Superfamily: bcl apoptosis regulator, inhibitory type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: bcl-x, a bcl-2-related gene that functions as a A;Reference number: A47537; MUID:93364977; PMID:8358789 A;Accession: A47537 A;Status: preliminary
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C;Superfamily: bcl
C;Keywords: B-cell
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                                                                                                                                                                                                                                                                                                                                                            LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDFWIQENGGWV
                                                                                                                                                                                                                                                                                                                                                                                                    LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELVIDEVSYKLSORGHCWSELEBEDENRTDTAAEABMDSVLNGSPSWHPPAGHVVNGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
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RESULT 15 B37332

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A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Residues: 1-214 <RES>
A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
C;Genetics:
C;Genetics:
A;Gene: bcl·x-long
C;Superfamily: bcl apoptosis regulator, inhibitory type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 28-Jul-2003
C;Accession: JE0203
C;Accession: JE0203
C;Accession: JE0203
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.
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A;Status: preliminary; translated
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C; Superfamily: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-227 <BAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: JE0203; MUID:98340865; PMID:9675101 A;Accession: JE0203
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Local Similarity 40.8%;
les 82; Conservation
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185
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                                                                                               81 QVSDELFQGGENWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                  66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                   29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                      11 RALVADFVGYKLROKGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
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                               SGGWAEFTALYGDGALEEARR 161
                                                                 QVVNELFRDGVNWGRIVAFFSFGGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELVVDFLSYKLSOKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
NGGWVRTKPLVCPFSLASGQR
                                                                                                                                                                                                     RELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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bcl apoptosis regulator,
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                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 377.5; l
Pred. No. 1.1e
16; Mismatches
                                                                                                                                                                                                                                                                                        Score 374.5;
Pred. No. 2.3
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 205
                                                                                                                                                                                                                                                                                                                                         inhibitory type
                                                                  CVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C;Accession: B37332; S35452
R,Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Accession: B37332; MUID:92375724; PMID:1508712
A;Accession: B37332
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Residues: 1-216 < EGU's
A;Cross-references: EMBL.D11381; EMBL:D11382
C;Superfamily: bcl apoptosis regulator, inhibitory type
Search completed: March 25, 2004, 15:45:07 Job time: 15 secs
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                                                                                                                                          145 AEFTA 149
                                                                                              190 VRACA 194
                                                                                                                                                                                           130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSFLVDNIATWMTEYLNRHLHNWIQDNGGW 189
                                                                                                                                                                                                                        85 ELFQGGDNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                  10 DNREIVLKYIHYKLSORGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                                                  70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                    Database
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                A_Geneseq_29Jan04:*
1: geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
                                                                            geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result No.	Score	% Query Match	Length	BU	ID	Description
1	1009	0 :	193	N	AAY05531	Mouse
N	1005	ø	193	N	AAW61391	w61391 Rat bcl-
ω	1005	9	193	N	AAW97391	The r
4	8	9	192	N	AAW97393	Prote
υī	1000	9	193	N	53	530 Human Bc
o	1000	9	193	7	4	Human
7	995	œ	193	N	AAW61392	392 Human
80	995	œ	193	N	9	Aaw97392 The human
9	993	œ	193	N	AAW36047	7 Human bo
10	993	œ	193	N	AAY05532	
11	990	œ	192	N	AAW97394	Mammalia
12	967.5	<u>ب</u>	192	N	AAY05533	Mouse
13	876	რ	168	N	AAW36048	Mouse bo
14	814.5	80.7	190	ຫ	AA018223	3 Human E
15	759	<u>ა</u>	365	N	AAW59884	Amino
16	759	5	365	ψ	ABG95556	Abg95556 Human nov
17	759	'n	365	9	ABO34750	gmer
18	443	'n	411	4	AAU00219	В
19	430.5	'n	237	ψı	ABG78480	) Wild
20	N)	Ņ	233	4.	AAB73303	
21	K)		233	7	ADE62921	2921
22	<b>N</b> 3	ν.	233	7	ADE62491	Ade62491 Rat Prote
23	K1		233	N	AAR68887	387
24	427.5	42.4	233	N	AAW05821	Aaw05821 Bcl-XL pr
25			233	N	AAW31530	Aaw31530 Human ant

The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Wethods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or mutine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w.

Claim 2; Page 35; 52pp; English.

45	44	43	42	41	40	υ 9	ც	37	3 6	35	34	33	32	31	30	29	28	27	ď
411.5	411.5	411.5	411.5	411.5	411.5	412	412	414.5	415.5	424.5	425	427.5	•	427.5	•	427.5	427.5	27.	•
٠	40.8	40.8	40.8	40.8	40.8	40.8	40.8	41.1	41.2	42.1	42.1	42.4	42.4	42.4	42.4	42.4	42.4	42.4	4.74
239	239	239	239	239	239	236	236	152	239	233	225	348	236	233	233	233	233	233	200
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AAU76553	ABG78478	ABG78479	AAB74127	AAB35130	AAW87810	AAU76554	AAB35131	AAG79760	AAG64037	AAB73304	AAW19396	ABR83557	ABR83558	ADE62493	AAB47515	AAG64262	AAB50538	AAY83223	0
Aau76553	Abg78478	Abg78479	Aab74127	Aab35130	Aaw87810	Aau76554	Aab35131	Aag79760	Aag64037	Aab73304	Aaw19396	Abr83557	Abr83558	Ade62493	Aab47515	Aag64262	سا	322	Tay out of
Human Bc.	Human Bcl	Human Bcl	Human	Human	A huma	Murine Bc			Human Bcl	Mutant ra	"Deprenyl	TOLA-BCL	TolA-BCL		Protei	Huma	i k		

# ALIGNMENTS

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RESULT 1
AAY05531
ID AAY0
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                                                    N-PSDB; AAX25133.
                                                                                                                                                                                                      Cory S,
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                                                                                                   WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1997;
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Best Local S
Matches 193
                               in the cell death pathway. The bcl-2 family have both apoptotic ac and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. antisense constructs can be used in disorders where prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                     Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g.
                                                                                                                                                                                                                                                                                                                                                                            bcl-y;
                                                                                                                                                                                                                                                                                                                                                                                                  Rat bcl-y protein.
Sequence
                                                                                                The mammalian
                                                                                                                      Example;
                                                                                                                                                                                                 WPI; 1998-446079/38
                                                                                                                                                                                                                       Guastella
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                       desired
                                                                                                                      Fig 3A; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein;
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                                                                                                bcl-y protein is a member of the bcl-2 family,
                                                                                                                                                                                                                                                                                                                                                                              cell death
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                                                                                                                                                                                                                                                                                        97US-00798897
                                                                                                                                                                                                                                             INC.
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Pred. No. 7
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1.4e-102;
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Query Match Best Local s

Local Similarity

99.6%; 99.5%;

Score 1005; DB 2; Pred. No. 2e-101;

Length 193;

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RESULT 3
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The present sequence represents rat bcl-y protein (Rbcl-y). The specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheiner's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasi
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                                                                                                                                                                                                                                Disclosure; Col 15-18; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                Guastella
                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
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                                                                                                                                                                                                                                                              modulating
                                                                                                                                                                                                                                                                                Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                              N-PSDB; AAX15945
                                                                                                                                                                                                                                                                                                                               WPI; 1999-214150/18.
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RESULT 4
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AC AAW97399
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y, bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; againg; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis) Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein sequence of the specification.
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                                                                                                                                                Disclosure; Col 19-20; 26pp; English
                                                                                                                                                                                                           modulating
                                                                                                                                                                                                                                   Novel bcl-y homologues of the rat and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1997;
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                                                                                                                                                                                                        programmed cell death.
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97US-00798897.
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Pred. No. 2e-101;
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                                                                                                                                                                                                                                      human bcl-2 protein - useful for
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Best Local :
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                                                                                           WPI; 1999-243890/20.
N-PSDB; AAX25132.
                                                                                                                                                                                                                                                                                                                            Spermatogenesis; animal model.
                                                                                                                                                                                                                                                                                                                                                                    Human Bcl-w protein essential
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05530;
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                                                                                                                                                                                        16-SEP-1997;
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                                                                                                                                                                                                                                                                                                  Homo sapiens
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Pred. No. 7.1e-101;
0; Mismatches 1;
                                                                                                                                    Gibson
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An animal model exhibiting reduced protein associated with Bcl-w.

levels

of a

Bcl-w

protein and/or

The present sequence is

human Bcl-w, English.

b

pro-survival member

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Bc1-2

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52pp;

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RESULT 6
ADD46742
ID ADD4
Query Match
Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a metho and to an animal model for the identification of molecules
                                                                                                                                                                                         14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
                                                                                                                                                                                                                                                                                                                                                                                                      Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic cons spared nerve injury; SNI; Chung.
                                                  WPI; 2003-268312/26.
GENBANK; Q92843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Protein Q92843,
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(FARB )
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ilarity 99.0%;
Conservative
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; Pred. No. 7.1e.
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        chronic constriction injury; CCI;
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                                                                                                       Costigan
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7.1e-101;
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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, contrivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence contrivative or allelic variation of the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying an agent the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound which regulates the activity of one or more of the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the polypuptides or their antibodies. The polynucleotide squence that regulates the activity in an animal of one or more of the polypuptides or their antibodies. The polynucleotide or the compound that polypuptides or their antibodies. The polynucleotide or the compound that injury (CCI) and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (Chung), chronic constriction the sequence data for this patent did not form part of the printed conspective two specification, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at the specification will shed not serve the condition of the printed conditions.
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Sequence
                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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181
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                                                                                                                                                                1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                               Similarity
                                                                                                                    FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
            GALVTVGAFFASK 193
                                                                        QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                    MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
GALVIVGAFFASK 193
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                               99.1%;
                                                                                                                                                                                                   1;
                                                                                                                                                                                                   Score 1000; DB 7;
Pred. No. 7.1e-101;
1; Mismatches 1;
                                                                                                                                                                                                                            Length 193;
                                                                                                                                                                                                      Indels
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                                                   180
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                                                                                                                             120
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RESULT 7
AAW61392
04-AUG-1998
                                                                       Human bcl-y protein.
                                                                                     02-OCT-1998
                                                                                                    AAW61392;
                                                                                                                 AAW61392 standard; protein; 193
11-FEB-1997;
                            US5789201-A.
                                           Homo sapiens
                                                        bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis;
                                                                                     (first entry)
97US-00798897
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New composition comprising preparing a medicament for

two or more isolated polypeptides, useful for treating pain in an animal.

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RESULT 8
AAW97
AAW9
XX AAW9
XX AAW9
XX The
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XX Rat
XX Rat
XX Pros
XX Pros
XX Pros
XX Homo
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Best Local (
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                                                                                                                                                                                                                                                             Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding B-cell lymphoma-y protein - useful recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guastella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense constructs can be used in disorders where prevention of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97392 standard; protein; 193
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                     Kaposi's sarcoma;
                                                               16-MAR-1999
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DB; AAV28334.
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                                                                                                                                                                                                                                     lung cancer; autoimmune; hyperimmune disease; parasite
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Pred. No. 2.5e-100;
1; Mismatches 2;
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190;

Conservative

1;

Indels

0;

Gaps

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The present sequence represents human bcl-y protein (Hbcl-y). The CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-CY are homologues of the bcl-2 protein thought to be involved in CY proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, CC aliabeth ymultiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of curiggers which may or may not be apparent. They may also be used in this certod. In contrast, if they act as cell death stimulators, Rbcl-y and CC these parallel to treat conditions associated with prolonged cell cand auto/hyperimmune diseases. They may also be used to cause cell death cause cell death for an extended conditions such as cancer (especially kaposi's sarcoma and lung cancer) ce in, and hence control, parasites
Query Match
Best Local S
Matches 190
                                                                            Sequence 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulating programmed cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel bcl-y homologues of the rat and human bcl-2 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX15946
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11-FEB-1997;
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                    Similarity
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97US-00798897.
                  98.6%;
  Score 995; DB 2; I
Pred. No. 2.5e-100;
1; Mismatches 2;
                                       Length 193;
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                                                                               QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                       FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                       MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
GALVTVGAFFASK 193
                            GALVIVGAFFASK 193
                                                           QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                      FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                 MATPASAPOTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                                                                                       120
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25-NOV-1997;

97US-00978523

RESULT 9
AAW36047
ID AAW3
XX
AC AAW3
XX
DT 22-A
XX
DT 41-A
XX
XX
DT 61-A
XX
XX
AC Huma
XX
XX
AC Homc
XX
AC Homc
XX
AC AAW3
AC

22-APR-1998

(first entry)

AAW36047;

AAW36047 standard; protein;

Human bcl-w protein.

Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.

Homo sapiens

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RESULT 10
AAY05532
ID AAY055
XX AAY05
XX AAY05
XX D5-JU
DT 05-JU
DX Human
XX Sperm
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Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a novel human protein, bol-w, encoded by the bol 2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding apoptosis related gene bcl-w - used to induce inhibit cell survival, e.g. for treatment of cancer and degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cory S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193 AA;
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                                                                                                   Spermatogenesis;
                                                                                                                                      Human Bcl-w protein essential
                                                                                                                                                                      05-JUL-1999
                                                                                                                                                                                                                                      AAY05532
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                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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                                                                                                                                                                                                                                                                                                                                                                                      QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
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                                                                                                       Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                    protein;
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                                                                                                                                                                      entry)
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Pred. No. 4.2e-100
2; Mismatches 2
                                                                                                                                    for spermatogenesis
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The present sequence is described of a derivative of human Bcl-w (see also AAY05530), a pro-survival member of the Bcl-2 family that is widely cexpressed and which is essential for spermatogenesis. The invention crelates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the creatment of infertility, or for reducing fertility, by modulating creatment of infertility, or for reducing fertility, by modulating creatment of the human or murine bcl-w gene (see AAX25132-35) or in a gene callele of the human or murine bcl-w gene (see AAX25132-35) or in a gene cassociated with bcl-w. Such animals have disorganised seminferous tubules as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, can induce inferritity.
                                      can
                                                                                                                                                                                                                                                                                                                                                              An animal model exhibiting reduced levels of a protein associated with Bcl-w.
Sequence 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1997;
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                                        induce infertility
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Best Local S
Matches 189
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181
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                                                                                                                                                                                 1 MATPASTPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                       Similarity
                                                                        QVQDWMVAYLETRLADWIHSSGGWABFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                      GALVIVGAFFASK 193
                                                                                                                              FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                         MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
 GALVIVGAFFASK 193
                                                 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                    FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                           98.4%;
llarity 97.9%;
Conservative
                                                                                                                                                                                                            2
                                                                                                                                                                                                           Score 993; DB 2;
Pred. No. 4.2e-100;
2; Mismatches 2;
                                                                                                                                                                                                                                   Length 193;
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RESULT 11
AAW97394
Mammalian bcl-y protein.
                                                               AAW97394 standard; protein; 192
                                            20-MAY-1999
                                            (first entry
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Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologu programmed cell death; apoptosis; necrosis; cell death inhibitor; stro head trauma; Alzheimer's Disease; necrosis; cell death; degenerative disease multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; homologue; disease; stroke;

WO9913710-A1

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RESULT 12
AAY05533
ID AAY05
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AC AAY05
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DT 05-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local &
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 05-JUL-1999
                                      AAY05533
                                                                   AAY05533 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1996;
11-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                     ALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                            ATPASTPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRTE
                                                                                                                                                                                                                                   VOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG
                                                                                                                                                                                                                                                                    VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
                                                                                                                                                                                                                                                                                                                                            SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
                                                                                                                                                               ALVIVGAFFASK 192
                                                                                                                                                                                                                                                                                                       SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ
                                                                                                                                                                                                                                                                                                                                                                             ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF
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(first entry)
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97US-00798897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192;
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RESULT 13
AAW36048
ID AAW36

AAW36048 standard; protein;

168

AAW36048

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The present sequence is described of a derivative of mouse Bcl-w (see CC also AAY(9531), a pro-survival member of the Bcl-2 family that is widely cxpressed and which is essential for spermatogenesis. The derivative clacks the 24 N-terminal amino acids of Bcl-w. The invention relates cc generally to a method of treatment and to an animal model for the cc identification of molecules and genetic sequences useful for inducing or creducing fertility of male animals. Methods are provided for the creatment of infertility, or for reducing fertility, by modulating cc spermatogenesis. An animal model carries a mutation is at least one cc allele of the human or mutaine bcl-w gene (see AAX25132-35) or in a gene cassociated with bcl-w. Such animals have disorganised seminferous tubules as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, the content of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 185; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhancing or otherwise facilitating spermatogenesis in animals, or which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39; 52pp; English.
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                                                                        GALVIVGAFFASK 193
                                                                                                                                                QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA~VSTVVTGAVAL
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GALVIVGAFFASK
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192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 967.5; DB 1
Pred. No. 2.5e-97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'nj
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RESULT 14
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Best Local Simi
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 168 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding apoptosis related gene inhibit cell survival, e.g. for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                     18-SEP-2002
                                                                                AAO18223
                                                                                                      AAO18223 standard;
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                               QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams
                                                                                                                                                                                                                                                    FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                       MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                        QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA
                                                                                                                                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                              MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50-51; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATIONS PTY LTD.
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                                                                                                      protein;
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                                                   entry)
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97.0%;
                           domain
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                           related
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Pred. No. 2.2e-87;
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                           protein
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                                                                                                                                                                                                                                                                                                                                                           Length 168
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Human; apoptotic signal transduction

protein; Bcl-Rambo; BHNo domain;

RESULT 15
AAW59884
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20-NOV-1998 AAW59884;

(first

0f entry)

the CDNA

clone

Bcl-like

(HAICH29)

AAW59884 standard;

protein;

365

B

Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; neuroprotective; antiparkinsonian; virucide; antiinf
immunosuppressive; anti-HIV; antibacterial; hepatotropic; septi
Parkinson's disease; muscular dystrophy; HIV; viral infection;
                                                                                                                                                                                                                                                                                                                         Seguence
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04-JAN-2001; 2001DE-01000280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; neurodegenerative disease; Alzheimer's disease; cytostatic;
nootropic; neuroprotective; antiparkinsonian; virucide; antiinflammatory;
immunosuppressive; anti-HIV; antibacterial; hepatotropic; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-2001; 2001WO-EP014597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding Bcl-Rambo protein, useful for treating e.g. tumors identifying therapeutic modulators of Bcl-Rambo function.
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178
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                                                                                                                                                                                                                                                                                                                          190
                                                                                      QVQDWWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                    MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                          FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
GALVIVGAFFASK 190
                            GALVTVGAFFASK 193
                                                             QXQEXMVAYLETXLAX - IHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGXPNWGXXXAFFVFGAAXCAESVNXEMEPLVG
                                                                                                                                                                                           MATPASAPXTXAXVAD-XGYKLRQKGYVNGAGPGXGPAAD-XHQAXRAAGXEFETRFXRT
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                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                       80.7%;
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Pred. No. 1.4e-80;
1; Mismatches 21
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Homo sapiens

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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                  Sequence 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies or tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-414099/35.
N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Rosen CA, Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1997;
21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC. (AUCK-) AUCKLAND UNISERVICES LTD.
121
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                                                                                                                                1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                QVQDWMVAYLETRLADWIHSSGGW 144
                                                        FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                        FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
 QVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                       75.2%; ilarity 98.6%; Conservative
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97US-0034205P.
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                                                                                                                                                                                    Score 759; DB 2; Length 365; Pred. No. 3.9e-74;
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Search completed: March 25, Job time : 52 secs

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